

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:18:01 ; Search time 21 Seconds  
(without alignments)

689,063 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MOAVDNLTSAPGNTSLCTRD.....SQDNKKKQGGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Issued Patents AA: \*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB pep: \*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB pep: \*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB pep: \*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB pep: \*  
5: /cgn2\_6/ptodata/1/iaa/6C COMB pep: \*  
6: /cgn2\_6/ptodata/1/iaa/6D COMB pep: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	US-08-852-824-2	Sequence 2, Appl1
2	823	46.3	333	US-09-221-456-2	Sequence 2, Appl1
3	823	46.3	333	US-09-558-740-2	Sequence 2, Appl1
4	797	44.8	333	US-08-812-871-1	Sequence 1, Appl1
5	772	43.4	325	US-08-467-948A-29	Sequence 29, Appl1
6	772	43.4	325	US-08-467-947A-29	Sequence 29, Appl1
7	772	43.4	338	US-08-988-876-8	Sequence 8, Appl1
8	772	43.4	338	US-09-303-524A-2	Sequence 2, Appl1
9	679.5	38.2	358	US-08-988-876-3	Sequence 3, Appl1
10	546.5	30.7	293	US-08-467-948A-6	Sequence 6, Appl1
11	546.5	30.7	293	US-08-467-947A-6	Sequence 6, Appl1
12	488	27.4	319	US-08-702-344-28	Sequence 28, Appl1
13	410.5	23.1	326	US-08-118-270-39	Sequence 39, Appl1
14	410.5	23.1	326	PCT-US93-08528-39	Sequence 39, Appl1
15	392.5	22.1	342	US-08-988-876-9	Sequence 9, Appl1
16	379.5	21.3	361	US-08-383-750-4	Sequence 4, Appl1
17	379.5	21.3	361	US-08-352-678-4	Sequence 4, Appl1
18	379.5	21.3	361	US-09-536-954-4	Sequence 4, Appl1
19	379.5	21.3	361	US-09-170-496D-78	Sequence 78, Appl1
20	379.5	21.3	361	US-09-170-496D-206	Sequence 206, Appl1
21	379.5	21.3	361	PCT-US93-09636-4	Sequence 4, Appl1
22	378	21.3	316	US-09-690-454-69	Sequence 69, Appl1
23	376	21.1	348	US-08-852-824-17	Sequence 17, Appl1
24	374.5	21.1	381	US-08-467-125-2	Sequence 2, Appl1
25	374.5	21.1	381	US-08-911-320A-2	Sequence 2, Appl1
26	374.5	21.1	381	US-09-217-101-2	Sequence 2, Appl1
27	349.5	19.7	302	US-08-467-948A-30	Sequence 30, Appl1

28	349.5	19.7	302	US-08-467-947A-30	Sequence 30, Appl1
29	347.5	19.5	346	US-09-585-876-2	Sequence 2, Appl1
30	339	19.1	344	US-08-467-948A-8	Sequence 8, Appl1
31	339	19.1	344	US-08-467-947A-8	Sequence 8, Appl1
32	337	19.0	68	US-08-905-223-327	Sequence 327, Appl1
33	332.5	18.7	339	US-09-170-496D-182	Sequence 182, Appl1
34	329.5	18.5	339	US-08-153-848-44	Sequence 44, Appl1
35	329.5	18.5	339	US-08-812-871-3	Sequence 3, Appl1
36	329.5	18.5	339	US-09-299-843A-44	Sequence 44, Appl1
37	329.5	18.5	339	US-09-088-337B-44	Sequence 44, Appl1
38	329.5	18.5	339	US-09-170-496D-32	Sequence 32, Appl1
39	329.5	18.5	339	PCT-US93-11153-44	Sequence 44, Appl1
40	329.5	18.5	339	PCT-US95-07180-2	Sequence 2, Appl1
41	329	18.5	359	US-08-041-219A-6	Sequence 6, Appl1
42	329	18.5	359	US-08-417-122-6	Sequence 6, Appl1
43	327.5	18.4	395	US-08-097-938-2	Sequence 2, Appl1
44	327.5	18.4	395	US-08-476-000-2	Sequence 2, Appl1
45	327.5	18.4	395	US-08-472-840-2	Sequence 2, Appl1

## ALIGNMENTS

RESULT 1  
US-08-852-824-2  
; Sequence 2, Application US/08852824C  
; Patent No. 6060272  
; GENERAL INFORMATION:  
; APPLICANT: Li et al.  
; TITLE OF INVENTION: Human G-Protein Coupled Receptors  
; FILE REFERENCE: 1488.1220000  
; CURRENT APPLICATION NUMBER: US/08/852,824C  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Genomic  
US-08-852-824-2

Query Match 100.0%; Score 1778; DB 3; Length 342;

Best Local Similarity 100.0%; Pred. No. 2.4e-144; Indels 0; Gaps 0;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MOAVDNLTSAPGNTSLCTRDYKITQVLPFLITYLVFVGLITNGLAMRIFPQIRKSNFI	60
DB	1	MOAVDNLTSAPGNTSLCTRDYKITQVLPFLITYLVFVGLITNGLAMRIFPQIRKSNFI	60
QY	61	IFLKNTVSDLMITFPFKLSDAKGTGGLTFVQCVSVIFPTMYISISFLGLITI	120
DB	61	IFLKNTVSDLMITFPFKLSDAKGTGGLTFVQCVSVIFPTMYISISFLGLITI	120
QY	121	DEYQKTRPFPKTSNPKNLGAKILSVIWMFPLISPNMLITNRQPRKXKCSFLKS	180
DB	121	DEYQKTRPFPKTSNPKNLGAKILSVIWMFPLISPNMLITNRQPRKXKCSFLKS	180
QY	181	BEGLYWHBIVNTICQVIVINFLVIVCYTILITELKSVYRTGVGVPRKKNVXKEI	240
DB	181	BEGLYWHBIVNTICQVIVINFLVIVCYTILITELKSVYRTGVGVPRKKNVXKEI	240
QY	241	IIAVFFICVPHFARIPYTLISQTEDEVDCTAENLTFYKESITLMTLSLNACDPFIYF	300
DB	241	IIAVFFICVPHFARIPYTLISQTEDEVDCTAENLTFYKESITLMTLSLNACDPFIYF	300
QY	301	ICKSPFNLSLWKCPNSATSLSQDNKKKQGGDPNEETPM 342	
DB	301	ICKSPFNLSLWKCPNSATSLSQDNKKKQGGDPNEETPM 342	

RESULT 2  
US-09-221-456-2  
; Sequence 2, Application US/09221456

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; Patent No. 6162899
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
; TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEA81 RECEPTOR
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,456
; FILING DATE: 28-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/956,975
; FILING DATE: 23-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70318-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-221-456-2

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Query Match 46.3%; Score 823; DB 3; Length 333;
Best Local Similarity 48.7%; Pred. No. 7.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKITQVLPFLLYTVLTVFVGLITNGLAMRIFFOIRKSNPFIIFLKNVTISDLIMILT 76
DB 15 CPRTRIVQLVFPALYTVVLTGILLNTLALWVHVHPSSSTFIILYKNTLVADLIMTLM 74

QY 77 FPFKILSDAKLGTGPTLRTFVCQVTSVIFYTMTWISIFLGLITIDRYOKTTRPKTSNPK 136
DB 75 LPFKILSDSHLAPWQLRAFAVCRFSSVIFYETMYGVIVLLGLIAFDPLKTIIRPLRNIFLK 134

QY 137 NLLGAKILSVVIWAFMFLLSLPNMLTNRDKNVKCKSFLKSEFGLVWHEIVNYICQV 196
DB 135 KPVFAKTVSIFWFFLFIISLPNTILSNKEATSSVKKCASLKGPLGKWHQVNNICQF 194

QY 197 IFWINFLVIVCYTLITKELYRSYVTRGVGKVPKKNVKKVFIITAVFFICVPPHFAF 256
DB 195 IFWTVFILMLVFYVVIKAKVYDSYRKSCKDKNNKKLEKGVFVWVAVFVCFAPHFAF 254

QY 257 IPYTLSDQTRDVFDCATNTLFFVKESTLWLTSLNACLDPIYFPLCKSPNSLSMLKCP 316
DB 255 VPYTHSQTNKTDCLQNQLFIKAKETTLFLAATNIMDPLIYIFLCKKFTKLPQW--G 312

QY 317 NSATSLSQDNKKEQD 332
DB 313 RKTASSQENHSSQTD 328

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RESULT 4
US-08-812-871-1
; Sequence 1, Application US/08812871
; Patent No. 5955303
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Gugler, Karl
; APPLICANT: Muzong Cheng
; TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
; TITLE OF INVENTION: PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto

```

```

RESULT 3
US-09-558-740-2
; Sequence 2, Application US/09558740
; Patent No. 6358695
; GENERAL INFORMATION:
; APPLICANT: SATHE, GANESH
; APPLICANT: HALSEY, WENDY
; APPLICANT: MUIR, ALISON
; APPLICANT: CHAMBERS, JON
; APPLICANT: SZEKERES, PHILIP
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE HNEA81 RECEPTOR
; FILE REFERENCE: GH-70318-2
; CURRENT APPLICATION NUMBER: US/09/558,740
; CURRENT FILING DATE: 2000-04-26
; PRIOR APPLICATION NUMBER: 08/956,975
; PRIOR FILING DATE: 1997-10-23
; PRIOR APPLICATION NUMBER: 09/221,456
; PRIOR FILING DATE: 1998-12-28
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-558-740-2

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Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 7.6e-63;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKITQVLPFLLYTVLTVFVGLITNGLAMRIFFOIRKSNPFIIFLKNVTISDLIMILT 76
DB 15 CPRTRIVQLVFPALYTVVLTGILLNTLALWVHVHPSSSTFIILYKNTLVADLIMTLM 74

QY 77 FPFKILSDAKLGTGPTLRTFVCQVTSVIFYTMTWISIFLGLITIDRYOKTTRPKTSNPK 136
DB 75 LPFKILSDSHLAPWQLRAFAVCRFSSVIFYETMYGVIVLLGLIAFDPLKTIIRPLRNIFLK 134

QY 137 NLLGAKILSVVIWAFMFLLSLPNMLTNRDKNVKCKSFLKSEFGLVWHEIVNYICQV 196
DB 135 KPVFAKTVSIFWFFLFIISLPNTILSNKEATSSVKKCASLKGPLGKWHQVNNICQF 194

QY 197 IFWINFLVIVCYTLITKELYRSYVTRGVGKVPKKNVKKVFIITAVFFICVPPHFAF 256
DB 195 IFWTVFILMLVFYVVIKAKVYDSYRKSCKDKNNKKLEKGVFVWVAVFVCFAPHFAF 254

QY 257 IPYTLSDQTRDVFDCATNTLFFVKESTLWLTSLNACLDPIYFPLCKSPNSLSMLKCP 316
DB 255 VPYTHSQTNKTDCLQNQLFIKAKETTLFLAATNIMDPLIYIFLCKKFTKLPQW--G 312

QY 317 NSATSLSQDNKKEQD 332
DB 313 RKTASSQENHSSQTD 328

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STATE: CA  
 COUNTRY: USA  
 ZIP: 94304  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSO for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/812,871  
 FILING DATE: Filed Herewith  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0237 US  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 333 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: MMLR3DT01  
 CLONE: 568987  
 US-08-812-871-1

Query Match 44.8%; Score 797; DB 2; Length 333;  
 Best Local Similarity 47.8%; Pred. No. 1.3e-60;  
 Matches 151; Conservative 57; Mismatches 106; Indels 2; Gaps 1;

QY 17 CTRDYKLTQVLPFLYLVFFVGLITNGLAMRIFFOIRKSNFIILKNTVLSLLMILT 76  
 DB 15 CPDRTRIVQVFPALYFVFLTGILLNLALWVFPVPSSTFIILKNTLVADLIMLT 74  
 QY 77 FPKILSDAKLGTGPLATFVCQVTSVIFFTMYISIFLGLITIDRYQKTRPPFKTSNPK 136  
 DB 75 LPPKILSDSLAPQLRAFCRFSVIFFTMYVIGVLLGLIAFDRLKIRPLRNIFLK 134  
 QY 137 NLGAKILSVVIAFWPFLSLPMLTNRQPRDNVKKSFLEGLVWHVIVYICQV 196  
 DB 135 KPVPKTVSIFVFFLFIPLMILSNKEATPSVKKCASLKGPLGLKWHQWNNICQF 194  
 QY 197 IFWNLFLIVVCVTLITKELYRSYVTRGVGKVRPKKVNKVFIIIAVFFICFVPPHAR 256  
 DB 195 IFWTLTLMVYVVIKAYVDSYKSKCKDRKNNKLBGVVVFVVFVCFAPHAR 254  
 QY 257 IPYTLSDTRDVEDCTAENTLFYKVESTLMTLSNACLDPPIYFLCKSPRNSLIMKCP 316  
 DB 255 VPYTHSTNNKTDCLQNLQFLAKETTLFLAATNICMDPLISIFLCKKTEKLPCMQ--G 312  
 QY 317 NSATLSQDNKKKQD 332  
 DB 313 RKITASSQENHSSQTD 328

RESULT 5  
 US-08-467-948A-29  
 ; Sequence 29, Application US/08467948A  
 ; Patent No. 5998164  
 ; GENERAL INFORMATION:  
 ; APPLICANT: LI, YI  
 ; APPLICANT: CAO, LIANG  
 ; APPLICANT: NI, JIAN  
 ; APPLICANT: GENTZ, REINER  
 ; APPLICANT: BULT, CAROL J.  
 ; APPLICANT: SUTTON III, GRANGER G.

APPLICANT: ROSEN, CRAIG A.  
 TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
 TITLE OF INVENTION: Coupled Receptor GPR2  
 NUMBER OF SEQUENCES: 30  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
 STREET: 1100 NEW YORK AVE., NW, SUITE 600  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC COMPATIBLE  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/467,948A  
 FILING DATE: 06-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US95/04079  
 FILING DATE: 30-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: STEFFE, ERIC K.  
 REGISTRATION NUMBER: 36,688  
 REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202-371-2600  
 TELEFAX: 202-371-2540  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 325 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: not relevant  
 MOLECULE TYPE: peptide  
 US-08-467-948A-29

Query Match 43.4%; Score 772; DB 2; Length 325;  
 Best Local Similarity 47.5%; Pred. No. 1.7e-58;  
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNSTLCTRDYKLTQVLPFLYLVFFVGLITNGLAMRIFFOIRKSNFIILK 65  
 DB 2 NSTQTPDSCSNLITQIIPVLYCMVFIAGILNGVGHIFVFPSSKFIILK 61  
 QY 66 TVISDLMLITFPFKILSDAKLGTGPLRTFVCQVTSVIFFTMYISIFLGLITIDRYK 125  
 DB 62 IVIADFVMSLTFPPKILGDSGLGPWQLNVPVCRVSAVLFVNNKYSIVFFGLISFDYRK 121  
 QY 126 TTRPFTSNPKLGLAKILSVIWAFWPFLSLPMLTNRQPRDNVKKSFLEGLV 185  
 DB 122 IVKPLTSTFQSVSYKSLSVIWMMLLAVNIIITNOSVREVTOIKIELKSELGRK 181  
 QY 186 WHEIVNYICQVIFWNLFLIVVCVTLITKELYRSYVTRGVGKVRPKKVNKVFIIIAV 245  
 DB 182 WKASNYIFVAIFWVFLIIVFYTAITKIFKSHLSSRNSTSVKCKSRNIFSVFV 241  
 QY 246 PICVPPHARIPYTLSDTRDVEDCTAENTLFYKVESTLMTLSNACLDPPIYFLCKSP 305  
 DB 242 FVCFVPYHARIPYTKSQTRAHVSQSKQKILRYMKSEFTLLLSAANVCLDPIYFLCKSP 301  
 QY 306 RNSLISMLKCNESA 319  
 DB 302 REILCKKLHLEPKA 315

RESULT 6  
 US-08-467-947A-29  
 ; Sequence 29, Application US/08467947A  
 ; Patent No. 6090575  
 ; GENERAL INFORMATION:

```

; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,947A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KIM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 325 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; US-08-467-947A-29

Query Match 43.4%; Score 772; DB 3; Length 325;
Best Local Similarity 47.5%; Pred. No. 1.7e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKLTQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFIILKN 65
DB 2 NSTSTQPPDESCQNLLITQOIIPVLCMVFTAGILLNGVSGWIFFYVPSSKSFIIYLN 61
QY 66 TWISDLMLITPFPKILSDAKLTGTPRTFVQVTSVIFPYFTMYISIFGLITIDRYOK 125
DB 62 IVIADPMSLTTPFKILGSDGLGPMQLNVFCVSAVLFYVNMYSIVFFGLISFDYYK 121
QY 126 TTRPFTKSNPKLLGAKILSVIWMFLLSPNMLTNRQPRDKNVKCSFLKSEFGLV 185
DB 122 IVKPLMTSFIQSVSYKLSVIVWMLLAVPNILITNQSVREVTQIKIELKSELGRK 181
QY 186 WHEIVNYICQVIFWIFNFIIVCYTILITKELYSYVTRGVGKVPKKNVVFIIIAVF 245
DB 182 WHKASNYIFVAIFWIFVFLIIIVFYTAITKKIFKSHLKSSRNSTSVKKSRRNIFSVFV 241
QY 246 FICFVPHFARIPTLTLSQTRDVFDCFTAENTLTVKKESTLWLTSLNACLDPPFYFLCKSF 305
DB 242 FVCVPHIARIPTLTLSQTRDVFDCFTAENTLTVKKESTLWLTSLNACLDPPFYFLCKSF 301
QY 306 RNSLISMLKCPNSA 319
DB 302 REILCKKGLHIPLKA 315

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RESULT 7
US-08-988-876-8
; Sequence 8, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; TITLE OF INVENTION: WITH IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/988,876
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0441 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 338 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 285995
; US-08-988-876-8

Query Match 43.4%; Score 772; DB 3; Length 338;
Best Local Similarity 47.5%; Pred. No. 1.7e-58;
Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKLTQVLPFLYTVLFFVGLITNGLAMRIPFQIRSKSNFIILKN 65
DB 3 NSTSTQPPDESCQNLLITQOIIPVLCMVFTAGILLNGVSGWIFFYVPSSKSFIIYLN 62
QY 66 TWISDLMLITPFPKILSDAKLTGTPRTFVQVTSVIFPYFTMYISIFGLITIDRYOK 125
DB 63 IVIADPMSLTTPFKILGSDGLGPMQLNVFCVSAVLFYVNMYSIVFFGLISFDYYK 122
QY 126 TTRPFTKSNPKLLGAKILSVIWMFLLSPNMLTNRQPRDKNVKCSFLKSEFGLV 185
DB 123 IVKPLMTSFIQSVSYKLSVIVWMLLAVPNILITNQSVREVTQIKIELKSELGRK 182
QY 186 WHEIVNYICQVIFWIFNFIIVCYTILITKELYSYVTRGVGKVPKKNVVFIIIAVF 245
DB 183 WHKASNYIFVAIFWIFVFLIIIVFYTAITKKIFKSHLKSSRNSTSVKKSRRNIFSVFV 242
QY 246 FICFVPHFARIPTLTLSQTRDVFDCFTAENTLTVKKESTLWLTSLNACLDPPFYFLCKSF 305

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Db 243 FVCVPVYHARIPTKQTEAHYSCSQKEILRYMKFTLLLSAANVCLDPIIYFLLCQPF 302  
 QY 306 RNSLSMLKCPNSA 319  
 Db 303 REILCKKLHIPLKA 316

RESULT 8

US-09-303-524A-2  
 ; Sequence 2, Application US/09303524A  
 ; Patent No. 6238873  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CHAMBERS, JONATHAN K.  
 ; APPLICANT: STEWART, BRIAN R.  
 ; APPLICANT: AMES, ROBERT S.  
 ; APPLICANT: SARAU, HENRY M.  
 ; APPLICANT: FOLEY, JIM  
 ; APPLICANT: ARNOLD, ANNE ROMANIC  
 ; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND  
 ; ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001  
 ; TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF  
 ; FILE REFERENCE: GP50007  
 ; CURRENT APPLICATION NUMBER: US/09/303,524A  
 ; CURRENT FILING DATE: 1999-04-30  
 ; PRIOR APPLICATION NUMBER: 60/083,957  
 ; PRIOR FILING DATE: 1998-05-01  
 ; NUMBER OF SEQ ID NOS: 2  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO: 2  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-303-524A-2

Query Match 43.4%; Score 772; DB 3; Length 338;  
 Best Local Similarity 47.5%; Pred. No. 1.7e-58;  
 Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKITQVLPVLYLVLPFVGLITNGLAMRIFPQIRSKSNFIILKXN 65  
 Db 3 NSTSQPPDESQNLITQIIPVLCVFIAGILLNGVSGWIFFYVPSSKSFIIYLN 62  
 QY 66 TVISDLMLTPFPKILSDAKLGTGPTLVFVQVTSVIFFTWISISFLGLITIDRYQK 125  
 Db 63 IVIAFVMSLTPFPKILSDGLGPNQVFCVRSVAVLFYNNVSVIFVGLISFDRYK 122  
 QY 126 TTRPFTSNPKNLLGAKILSVVIVAFMFLSLPNNMILTNQPRDKNVKCSFLKSEFGLV 185  
 Db 123 IVKPLWTSFIQSVSKLSLVIVVMMLLAVPNIILTNQSVREVTQIKCIELKSELGRK 182  
 QY 186 WHEIYNYICQVIFWNLIVIVCVTLITKELYSVVRTRGVKVPKKNVKKVFIIVAF 245  
 Db 183 WKAASNYIFVAIFWVFLVLLVFIYTAITKFKSHLKSRSNSTSVKKSSRNISIVFV 242  
 QY 246 FICFVFPFHARIPYTLQTRDVEDCTAENTLFPYVKESTLWLTSLNACLDPIIYFLLCKSF 305  
 Db 243 FVCVPVYHARIPTKQTEAHYSCSQKEILRYMKFTLLLSAANVCLDPIIYFLLCQPF 302  
 QY 306 RNSLSMLKCPNSA 319  
 Db 303 REILCKKLHIPLKA 316

RESULT 9

US-08-988-876-3  
 ; Sequence 3, Application US/08988876  
 ; Patent No. 6063596  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lal, Preeti  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Hillman, Jennifer L.  
 ; APPLICANT: Yue, Henry

; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
 ; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSeq for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/988,876  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0441 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 358 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: PROSTUT09  
 ; CLONE: 1650519  
 ; US-08-988-876-3

Query Match 38.2%; Score 679.5; DB 3; Length 358;  
 Best Local Similarity 43.7%; Pred. No. 1.4e-50;  
 Matches 132; Conservative 64; Mismatches 99; Indels 7; Gaps 4;

QY 6 NLTSAPG-NTSLCTRDYKITQVLPVLYLVLPFVGLITNGLAMRIFPQIRSKSNFIILK 64  
 Db 25 NRSDFGKNTLL--HNEPDTIVLPVLYLIFVASILLNGLAVIFFHIRNKTISIFVLK 81  
 QY 65 NTVISDLMLTPFPKILSDAKLGTGPTLVFVQVTSVIFFTWISISFLGLITIDRYQ 124  
 Db 82 NIYVADLIMTLTFFPPIVHDAGFGPWYFKILCRYTSLFYANMYTSIVFLGLISIDRYL 141  
 QY 125 KTRPFTSNPKNLLGAKILSVVIVAFMFLSLPNNMILTNQPRDKNVKCSFLKSEFGL 184  
 Db 142 KVKPFGDGRMYSIFTKVLSVCVVMVAVLSLPNILLTNGOPTEDNTHDCSKLSPGV 201  
 QY 185 WHEIYNYICQVIFWNLIVIVCVTLITKELYSVVRTRGVKVPK-KVNVKVFIIIA 243  
 Db 202 KWTAVTVYNSCLFVAVLVILICVIAISRYTHKS--SEQFISQSSRKKHNSIRVVA 259  
 QY 244 VFICFVFPFHARIPYTLQTRDVEDCTAENTLFPYVKESTLWLTSLNACLDPIIYFLLCK 303  
 Db 260 VYFTCLPVLHLCMPSTFSLDRLLDESQAQILYYCKEITLFLSACNVCLDPIIYFFMCR 319  
 QY 304 SF 305  
 Db 320 SF 321

RESULT 10  
 US-08-467-948A-6  
 ; Sequence 6, Application US/08467948A

Patent No. 5998164  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR2  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,948A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-948A-6

Query Match 30.7%; Score 546.5; DB 2; Length 293;  
Best Local Similarity 42.3%; Pred. No. 2.6e-39;  
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;  
QY 17 CTRDYKITQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLMLILT 76  
DB 15 CPKDTRIQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLMLILT 74  
QY 77 FPKILSDAKLGTGLRTFCVQTSVIFVFTWYISISFLGLITIDRYOKTTRPFTSNPK 136  
DB 75 LPPKILSDHLAPQWLRARVCFSSVIFVFTWYISISFLGLITIDRYOKTTRPFTSNPK 134  
QY 137 NLIGAKILSVVWAFMFLSLPNMILTRQPRDKNVKCSFLKSEFGLVWHEIVNYICQV 196  
DB 135 KPVGKTVSIFVFWFFISLPNMLSNKEATPSSVKKCASLKGPLGKWHQWNNICQF 194  
QY 197 IFWINFLVIVCVTLITKE-----LYRSYVTRGVGVKPKKVNKVFIIIAVFFICFVP- 251  
DB 195 IFWTVFIMLVFVVIYAKKIMILIESPKVTRTKTKSKAKYLLSWLSLCLVLLHFISPE 254  
QY 252 FHPARPYTLISQTRDVFDCDAENTLFPYVKESTLW 285  
DB 255 FHILTVPKPIRLT---VDCKI-NCILLKKQLSFW 284

RESULT 11  
US-08-467-947A-6

Sequence 6, Application US/08467947A  
Patent No. 6090575  
GENERAL INFORMATION:  
APPLICANT: LI, YI  
APPLICANT: CAO, LIANG  
APPLICANT: NI, JIAN  
APPLICANT: GENTZ, REINER  
APPLICANT: BULT, CAROL J.  
APPLICANT: SUTTON III, GRANGER G.  
APPLICANT: ROSEN, CRAIG A.  
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein  
TITLE OF INVENTION: Coupled Receptor GPR1  
NUMBER OF SEQUENCES: 30  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.  
STREET: 1100 NEW YORK AVE., NW, SUITE 600  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY DISK  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/467,947A  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/04079  
FILING DATE: 30-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: STEFFE, ERIC K.  
REGISTRATION NUMBER: 36,688  
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2540  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 293 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-467-947A-6

Query Match 30.7%; Score 546.5; DB 3; Length 293;  
Best Local Similarity 42.3%; Pred. No. 2.6e-39;  
Matches 116; Conservative 45; Mismatches 104; Indels 9; Gaps 4;  
QY 17 CTRDYKITQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLMLILT 76  
DB 15 CPKDTRIQVLPFLTYLVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLMLILT 74  
QY 77 FPKILSDAKLGTGLRTFCVQTSVIFVFTWYISISFLGLITIDRYOKTTRPFTSNPK 136  
DB 75 LPPKILSDHLAPQWLRARVCFSSVIFVFTWYISISFLGLITIDRYOKTTRPFTSNPK 134  
QY 137 NLIGAKILSVVWAFMFLSLPNMILTRQPRDKNVKCSFLKSEFGLVWHEIVNYICQV 196  
DB 135 KPVGKTVSIFVFWFFISLPNMLSNKEATPSSVKKCASLKGPLGKWHQWNNICQF 194  
QY 197 IFWINFLVIVCVTLITKE-----LYRSYVTRGVGVKPKKVNKVFIIIAVFFICFVP- 251  
DB 195 IFWTVFIMLVFVVIYAKKIMILIESPKVTRTKTKSKAKYLLSWLSLCLVLLHFISPE 254  
QY 252 FHPARPYTLISQTRDVFDCDAENTLFPYVKESTLW 285  
DB 255 FHILTVPKPIRLT---VDCKI-NCILLKKQLSFW 284

RESULT 12

Query Match	23.1%;	Score	410.5;	DB.1;	Length	326;			
Best Local Similarity	32.2%;	Pred. No.	1.2e-27;						
Matches	106;	Conservative	65;	Mismatches	137;	Indels	21;	Gaps	9;
QY	27	LPFLYTVLFFVGLITNGLAMRIFQI-RSKNFI-IPLKNTVISDMLMILFPPKILSD	84						
DB	1	LPFIVISIFVLGIITANGVLVFAFLPFSKNEKIFMWNLTVDLLELITLPLWIVY	60						
QY	85	AKLGGPLRTFFCVQTSVIFYFTWYISISFLGLITIDRYQKTRRPKTSNPKNLLGAKIL	144						
DB	61	SNQGNWLPKFLCNLAGCLFFINTYCSVAFLGVITNRFQAVKYPKTAQAATRKEGIAL	120						
QY	145	SVVIW-----AFNFIILSUPMILNRPDRKNVKCSFLKSEFG-----LVWHEIVNYIC	194						
DB	121	SLIVIVVAIVAAASYFLVMDSFNVSNKAGSNITRC-FERYEKSGKPLVIITH-----IC	174						
QY	195	QVI-FWINFLIVIVCVTLITKELYSYVTRGVGVKPKVNVKFIITIAVFICFVPH	253						
DB	175	IVLGGFIVFLFLFCNLVIITLLHLPQVQQRNAEV-RRALWMVCTVIANFVICEVPH	233						
QY	254	FARIIVYTLSQTRDFVDCDAENTLFVYKESTLWLTSLNACLDPFIYFFLCKSPFNLSIML	313						
DB	234	MYVLEPWTIAEL-GWPPSSNHOAINDAHQVTLGLSTNCVLDPVIYCFLTKKPKHLSEKL	292						
QY	314	KCPNATSLSQNRKKEQDGGDPNNEETPM	342						
DB	293	NIMRSSQKSRVTRDTGTGTEMAIPINHTPV	321						

## RESULT 14

PCT-US93-08528-39  
; Sequence 39, Application PC/TUS9308528  
; GENERAL INFORMATION:  
; APPLICANT: New York University  
; TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN  
; TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF  
; NUMBER OF SEQUENCES: 348  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08528  
; FILING DATE: 09-SEP-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/943,236  
; FILING DATE: 10-SEP-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, Kevin G.  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: MURPHY=2 PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 39:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 326 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
PCT-US93-08528-39

Query Match 23.1%; Score 410.5; DB 5; Length 326;  
Best Local Similarity 32.2%; Pred. No. 1.2e-27;  
Matches 106; Conservative 65; Mismatches 137; Indels 21; Gaps 9;

QY	27	LPFLYTVLFFVGLITNGLAMRIFFQI--RKSNTI-IFLKNVTISDLMLITPPFKILSD	84
Db	1	LPPIVYIIFVLGIANGVLMVFWPARLYPSKKEIKIFMWNLTVADLLFLITLPLWIVY	60
QY	85	AKLGTGRLRTFVCOVTSVIFFTWYISIFLGLITIDRYOKTTRPFKTSNPKNLGAKIL	144
Db	61	SNQGNWFLPKFLCNLAGCLFFINTYCSVAFGLVITNRFQAVKYPKTAQATTKRGIAL	120
QY	145	SVIIV-----AFMFLSLPNMLNRPDRKNVKKCSFLKSEFG-----LWHEIVNYIC	194
Db	121	SLVIWVAIAAASYFLVWMDSTNVVSNKAGSNITRC--FEYERKSKPVLIIH-----IC	174
QY	195	QVI--FWINFLIIVCVTLITKELYSYVTRGVKVPKKNVKNVFLIIAIVFFICFVPEH	253
Db	175	IVLGFVIFVLLIFCNLVIHTLARGPVKQBNAEV--RRALWMVCTVIATVFCVPHH	233
QY	254	FARIPTYSQTRDVEDCTAENTLFVYKSTLWLTSLNACLDPPFYFFICKSFRNLSIML	313
Db	234	MYQLPWTIAEL--GMWPSNHQAINDAHQVTLCLLSTNCVLDPPVICYFLTKKFKHLSKL	292
QY	314	KCFNSATSLSDNRKKEQDGGPNSETPM	342
Db	293	NIMRSSQKCSRVRTDGTGEMAIPIINHIVP	321

## RESULT 15

US-08-988-876-9  
; Sequence 9, Application US/08988876  
; Patent No. 6063596  
; GENERAL INFORMATION:  
; APPLICANT: Lal, Preeti  
; APPLICANT: Bandman, Olga  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Yue, Henry  
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED  
; TITLE OF INVENTION: WITH IMMUNE RESPONSE  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/988,876  
; FILING DATE: Herewith  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PP-0441 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 9:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 342 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GenBank  
; CLONE: 49443  
US-08-988-876-9

Query Match 22.1%; Score 392.5; DB 3; Length 342;  
Best Local Similarity 30.7%; Pred. No. 4.3e-26;  
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY	20	DYKITQVLPFLYTVLFFVGLITNGLAMRIFFQI--RKSNTI-IFLKNVTISDLMLIT	76
Db	10	DSEFRYTFPIVYIIFVLGIANGVLMVFWPARLYPSKKEIKIFMWNLTVADLLFLIT	69
QY	77	FPFKILSDAKLGTGRLRTFVCOVTSVIFFTWYISIFLGLITIDRYOKTTRPFKTSNPK	136
Db	70	LPLWIVVYSNQGNWFLPKFLCNLAGCLFFINTYCSVAFGLVITNRFQAVKYPKTAQAT	129
QY	137	NLGLKILSVIIV-----AFMFLSLPNMLNRPDRKNVKKCSFLKSEFG-----LVWH	187
Db	130	TKRGIALSLVIWVAIAAASYFLVWMDSTNVVSNKAGSNITRC--FEYERKSKPVLIIH	188
QY	188	EIVNYICQVI--FWINFLIIVCVTLITKELYSYVTRGVKVPKKNVKNVFLIIAIVFF	246
Db	189	-----ICIVLGFVIFVLLIFCNLVIHTLARGPVKQBNAEV--RRALWMVCTVIATV	242
QY	247	ICFVPEHFAPIPTYSQTRDVEDCTAENTLFVYKSTLWLTSLNACLDPPFYFFICKSFR	306



Db 243 ICFVPHMVQLPWTIAEL-GWPPSSNHQAINDAHQVTLCLLSTNCVLDPVYICFLTKKFR 301  
Qy 307 NSLISMLKCPNSATSLSDNRKKEQDGGDNEETPM 342  
Db 302 KHLSEKLNIMRSSQKCSRVTDTGTETMAIPINHPV 337

Search completed: February 4, 2004, 14:23:34  
Job time : 22 secs

GenCore version 5.1.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 14:22:16 ; Search time 37 Seconds  
(without alignments)  
1935.371 Million cell updates/sec

Title: US-09-780-576-2  
Perfect score: 1778  
Sequence: 1 MQAVNLTSAFGNTSLCTRD.....SQDNKKKQDGDPEHEETPM 342

Scoring table: BLOSUM62  
Gapop 10.0 , Capext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database : Published Applications AA:

- 1: /cgn2\_6/prodata/1/pubpaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/prodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/prodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/prodata/1/pubpaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/prodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/prodata/1/pubpaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/prodata/1/pubpaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/prodata/1/pubpaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/prodata/1/pubpaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/prodata/1/pubpaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/prodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/prodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/prodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/prodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/prodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/prodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
- 17: /cgn2\_6/prodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/prodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	9	US-09-835-922-2
2	1778	100.0	342	9	US-09-827-937A-2
3	1778	100.0	342	9	US-09-780-576-2
4	1778	100.0	342	10	US-09-964-008-1
5	1778	100.0	342	12	US-10-272-983-32
6	1778	100.0	342	12	US-09-745-842-6
7	1778	100.0	342	12	US-10-393-807-32
8	1778	100.0	342	12	US-10-417-820A-34
9	1778	100.0	342	15	US-10-225-567A-643
10	1778	100.0	342	15	US-10-333-844-2
11	1748	98.3	342	10	US-09-964-008-3
12	1634	91.9	315	12	US-09-745-842-4
13	1528.5	86.0	343	12	US-09-745-842-2
14	1237.5	69.6	267	12	US-09-745-842-12
15	829	46.6	333	11	US-09-924-125-2

16	829	46.6	333	11	US-09-957-187-2	Sequence 2, Appli
17	829	46.6	333	12	US-10-352-684A-34	Sequence 34, Appli
18	829	46.6	333	12	US-10-308-968-2	Sequence 2, Appli
19	829	46.6	333	15	US-10-243-106-2	Sequence 2, Appli
20	829	46.6	333	15	US-10-189-576-2	Sequence 2, Appli
21	829	46.6	333	15	US-10-225-567A-514	Sequence 514, App
22	823	46.3	333	9	US-09-769-159-2	Sequence 2, Appli
23	823	46.3	333	12	US-10-272-983-18	Sequence 18, Appl
24	823	46.3	333	12	US-10-393-807-18	Sequence 18, Appl
25	823	46.3	333	12	US-10-408-572-2	Sequence 20, Appl
26	823	46.3	333	12	US-10-417-820A-20	Sequence 20, Appl
27	797	44.8	333	9	US-09-848-889-1	Sequence 1, Appli
28	797	44.8	333	12	US-10-100-982-1	Sequence 1, Appli
29	772	43.4	338	15	US-10-024-494-29	Sequence 29, Appl
30	772	43.4	338	10	US-09-919-497-77	Sequence 77, Appl
31	772	43.4	338	12	US-09-745-842-13	Sequence 13, Appl
32	772	43.4	338	12	US-10-352-684A-42	Sequence 42, Appl
33	772	43.4	338	15	US-10-121-101B-10	Sequence 10, Appl
34	772	43.4	338	15	US-10-225-567A-213	Sequence 213, App
35	741.5	41.7	338	9	US-09-826-508-20	Sequence 20, Appl
36	694.5	39.1	358	9	US-09-826-508-10	Sequence 10, Appl
37	694.5	39.1	358	12	US-09-741-783-1	Sequence 1, Appli
38	694.5	39.1	358	12	US-10-295-027-364	Sequence 364, App
39	694.5	39.1	358	12	US-10-295-027-1255	Sequence 1255, Ap
40	694.5	39.1	358	15	US-10-225-567A-418	Sequence 418, App
41	679.5	38.2	358	10	US-09-919-172-22	Sequence 22, Appl
42	679.5	38.2	358	10	US-09-974-298-86	Sequence 86, Appl
43	679.5	38.2	358	15	US-10-121-101B-1	Sequence 1, Appli
44	549.5	30.9	314	12	US-10-264-237-2586	Sequence 2586, Ap
45	546.5	30.7	293	15	US-10-024-494-6	Sequence 6, Appli

## ALIGNMENTS

RESULT 1  
US-09-835-922-2  
; Sequence 2, Application US/09835922  
; Patent No. US20010046497A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Fang L.  
; APPLICANT: Luo, Lin  
; APPLICANT: Gustafson, Eric  
; APPLICANT: Liu, Fan-Hui  
; APPLICANT: Chen, Guodong  
; TITLE OF INVENTION: G-Protein Coupled Receptor and Methods  
; FILE REFERENCE: CN01167K  
; CURRENT APPLICATION NUMBER: US/09/835,922  
; CURRENT FILING DATE: 2001-04-16  
; PRIOR APPLICATION NUMBER: US 60/199,041  
; PRIOR FILING DATE: 2000-04-21  
; NUMBER OF SEQ ID NOS: 2  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: homo sapiens  
US-09-835-922-2

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Best Local Similarity	100.0%	Pred. No. 8.1e-159		
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QY	61	IFLKNVTISDLMLITPFFKILSDAKLGTGRLPFCQVTSVIFFTWYISISPLGITI	120	
Db	61	IFLKNVTISDLMLITPFFKILSDAKLGTGRLPFCQVTSVIFFTWYISISPLGITI	120	
QY	121	DRYQKTEPFKTSNPKNLGAKILSVIWAFFLISLPNMLITNRPQDKNKKCSFLKS	180	

Db 121 DRYQKTRPFTSNPKNLLGAKILSVVWVWAFMFLSLNNMLTNQPRDKNVKKSFLKS 180  
 Qy 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYRSVYRTRGVGVKPRKKNVNVKFI 240  
 Db 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYRSVYRTRGVGVKPRKKNVNVKFI 240  
 Qy 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFIYFF 300  
 Db 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFIYFF 300  
 Qy 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
 Db 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 2  
 US-09-827-937A-2  
 ; Sequence 2, Application US/09827937A  
 ; Patent No. US20020052043A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Li, Yi  
 ; APPLICANT: Ruben, Steven M.  
 ; TITLE OF INVENTION: Human G-Protein Coupled Receptors  
 ; FILE REFERENCE: 1488.1220003  
 ; CURRENT APPLICATION NUMBER: US/09/827,937A  
 ; CURRENT FILING DATE: 2001-04-09  
 ; PRIOR APPLICATION NUMBER: 08/852,824  
 ; PRIOR FILING DATE: 1997-05-07  
 ; NUMBER OF SEQ ID NOS: 18  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-827-937A-2

Query Match 100.0%; Score 1778; DB 9; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Qy 61 IFLKNTVISDLMLITPFPKILSDAKLGTGRLTFVQCQVTSVIFFTWYISISFLGLITI 120  
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 Db 121 DRYQKTRPFTSNPKNLLGAKILSVVWVWAFMFLSLNNMLTNQPRDKNVKKSFLKS 180  
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 Db 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYRSVYRTRGVGVKPRKKNVNVKFI 240  
 Qy 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFIYFF 300  
 Db 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFIYFF 300  
 Qy 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
 Db 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 3  
 US-09-780-576-2  
 ; Sequence 2, Application US/09780576  
 ; Patent No. US20020072072A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Civealli, Olivier  
 ; APPLICANT: No. US20020072072A1hacker, Hans-Peter  
 ; APPLICANT: Wang, Zhiwei

; APPLICANT: Reinscheid, Rainer  
 ; TITLE OF INVENTION: ADP-Glucose Receptor  
 ; FILE REFERENCE: P-UC 4530  
 ; CURRENT APPLICATION NUMBER: US/09/780,576  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/234,025  
 ; PRIOR FILING DATE: 2000-09-20  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-780-576-2

Query Match 100.0%; Score 1778; DB 9; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
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Qy 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFI 60  
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 Qy 61 IFLKNTVISDLMLITPFPKILSDAKLGTGRLTFVQCQVTSVIFFTWYISISFLGLITI 120  
 Db 61 IFLKNTVISDLMLITPFPKILSDAKLGTGRLTFVQCQVTSVIFFTWYISISFLGLITI 120  
 Qy 121 DRYQKTRPFTSNPKNLLGAKILSVVWVWAFMFLSLNNMLTNQPRDKNVKKSFLKS 180  
 Db 121 DRYQKTRPFTSNPKNLLGAKILSVVWVWAFMFLSLNNMLTNQPRDKNVKKSFLKS 180  
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 Db 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYRSVYRTRGVGVKPRKKNVNVKFI 240  
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 Db 241 IIAVFFICFVPHFARIPYTLISQTRDVFDCDAENTLFFVKESTLWLTSLNACLDPFIYFF 300  
 Qy 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
 Db 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 4  
 US-09-964-008-1  
 ; Sequence 1, Application US/09964008  
 ; Patent No. US20020156246A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Glucksmann, Maria A.  
 ; APPLICANT: Gu, Wei  
 ; TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1e1 G-Protein Coupled Recept  
 ; FILE REFERENCE: 5800-13, 035800-171548  
 ; CURRENT APPLICATION NUMBER: US/09/964,008  
 ; CURRENT FILING DATE: 2001-09-26  
 ; PRIOR APPLICATION NUMBER: 09/187,134  
 ; PRIOR FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 1  
 ; LENGTH: 342  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-964-008-1

Query Match 100.0%; Score 1778; DB 10; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
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DB 241 IIAVFFICFVPPHAPRIPYTLSTQTRVDFDCTAENTLFFYKESLWLTSLNACLDPIYFF 300  
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DB 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342

## RESULT 5

US-10-272-983-32  
; Sequence 32, Application US/10272983  
; Publication No. US20030148450A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/272,983  
; PRIOR FILING DATE: 2002-10-17  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 32  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-272-983-32

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches -0; Indels 0; Gaps 0;

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DB 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
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DB 181 EFGVLWHEIWNVICQVIFWFLNFIIVCVTLITKELYRSYVTRGVGVKPRKKNVKKVFI 240  
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DB 241 IIAVFFICFVPPHAPRIPYTLSTQTRVDFDCTAENTLFFYKESLWLTSLNACLDPIYFF 300  
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DB 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342

## RESULT 6

US-09-745-842-6  
; Sequence 6, Application US/09745842  
; Publication No. US20030170777A1  
; GENERAL INFORMATION:  
; APPLICANT: Conley, Pamela B.  
; APPLICANT: Jantzen, Hans-Michael  
; APPLICANT: Ramakrishnan-DuBridge, Vanitha  
; APPLICANT: Julius, David  
; APPLICANT: Hollopetter, Gunter  
; APPLICANT: COR Therapeutics, Inc.  
; TITLE OF INVENTION: P2Y12 Receptor  
; FILE REFERENCE: 44481-5053-US  
; CURRENT APPLICATION NUMBER: US/09/745,842  
; PRIOR FILING DATE: 2000-12-26  
; PRIOR APPLICATION NUMBER: US 60/171,622  
; PRIOR FILING DATE: 1999-12-23  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-745-842-6

Query Match 100.0%; Score 1778; DB 12; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 IFLKNTVISDLLMLTFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
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DB 241 IIAVFFICFVPPHAPRIPYTLSTQTRVDFDCTAENTLFFYKESLWLTSLNACLDPIYFF 300  
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DB 301 LCKSFNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342

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RESULT 7
US-10-393-807-32
; Sequence 32, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 32
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-393-807-32

Query Match 100.0%; Score 1778; DB 12; Length 342;
Best Local Similarity 100.0%; Pred. No. 8.1e-159;
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QY 61 IFLNKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
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RESULT 8
US-10-417-820A-34
; Sequence 34, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 155
; SOFTWARE: Patent In version 3.2
; SEQ ID NO 34
; LENGTH: 342
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-417-820A-34

Query Match 100.0%; Score 1778; DB 12; Length 342;
Best Local Similarity 100.0%; Pred. No. 8.1e-159;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60
DB 1 MQAVNLTSPAGNTSLCTRDYKITQVLPFLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60

QY 61 IFLNKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120
DB 61 IFLNKNTVISDLLMILTPFPKILSDAKLGTGPLRTFVCQVTSVIFFTWYISISFLGLITI 120

QY 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKXKCSFLKS 180
DB 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKXKCSFLKS 180

QY 181 EFLGVWHEIVNYICQVIFWINFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240
DB 181 EFLGVWHEIVNYICQVIFWINFLIVVCYTLITKELYSYVTRGVGVPRKKNVKVFI 240

QY 241 IIAVFFICVPPHFARIPTYLSQTRDVFDCYTAENTLFYVKESTLWLTSLNACLDPIFF 300
DB 241 IIAVFFICVPPHFARIPTYLSQTRDVFDCYTAENTLFYVKESTLWLTSLNACLDPIFF 300

QY 301 LCKSFNSLSMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342
DB 301 LCKSFNSLSMLKCPNSATSLSQDNRKKEQDGGDPNEETPM 342

RESULT 9
US-10-225-567A-643
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; Sequence 643, Application US/10225567A  
; Publication No. US20030113798A1  
; GENERAL INFORMATION:  
; APPLICANT: Lifespan Biosciences  
; APPLICANT: Brown, Joseph P.  
; APPLICANT: Burmer, Glenna C.  
; APPLICANT: Roush, Christine L.  
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 1920-4-4  
; CURRENT APPLICATION NUMBER: US/10/225,567A  
; CURRENT FILING DATE: 2001-12-19  
; PRIOR APPLICATION NUMBER: 60/257,144  
; PRIOR FILING DATE: 2000-12-19  
; NUMBER OF SEQ ID NOS: 2292  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 643  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-225-567A-643

Query Match 100.0%; Score 1778; DB 15; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
DB 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
QY 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
DB 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
QY 301 LCKSPRNSLISMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342  
DB 301 LCKSPRNSLISMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342

RESULT 11  
US-09-964-008-3  
; Sequence 3, Application US/09964008  
; Patent No. US20020156246A1  
; GENERAL INFORMATION:  
; APPLICANT: Glucksmann, Maria A.  
; APPLICANT: Gu, Wei  
; TITLE OF INVENTION: 15625 Receptor, A No. US20020156246A1 G-Protein Coupled Recept  
; FILE REFERENCE: 5800-13, 035800-171548  
; CURRENT APPLICATION NUMBER: US/09/964,008  
; CURRENT FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: 09/187,134  
; PRIOR FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 3  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Macaca sp.  
US-09-964-008-3

Query Match 98.3%; Score 1748; DB 10; Length 342;  
Best Local Similarity 98.0%; Pred. No. 5.3e-156;  
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
DB 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
QY 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
DB 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
QY 301 LCKSPRNSLISMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342

Query Match 100.0%; Score 1778; DB 15; Length 342;  
Best Local Similarity 100.0%; Pred. No. 8.1e-159;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
DB 61 IFLKNTVISDLLMLITPPFKILSDAKLGTGRLTFVQCQTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
DB 121 DRYQKTRPPKTSNPKNLLGAKILSVIWAFFLLSLPNMILTNRPDRDNKVKCSFLKS 180  
QY 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
DB 181 EFGLVWHEIVNYICOVIFWIFNFIIVCYTLITKELYSYVTRGVGVKPRKKNVVKVFI 240  
QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIFYFF 300  
QY 301 LCKSPRNSLISMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342

US-10-333-844-2  
; Sequence 2, Application US/10333944  
; Publication No. US20030124626A1  
; GENERAL INFORMATION:  
; APPLICANT: Yamanouchi Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: Method for screening antiplatelet agents  
; FILE REFERENCE: Y0122PCT-656  
; CURRENT APPLICATION NUMBER: US/10/333,844  
; CURRENT FILING DATE: 2003-01-24  
; PRIOR APPLICATION NUMBER: JP 2000-334721  
; PRIOR FILING DATE: 2000-11-01  
; PRIOR APPLICATION NUMBER: JP 2001-3577  
; PRIOR FILING DATE: 2001-01-11  
; NUMBER OF SEQ ID NOS: 12  
; SEQ ID NO 2  
; LENGTH: 342  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-333-844-2

Db 301 LCKSFRNSLSMLKCPNSATSQSDNRKKBQDGGDPNEETPM 342

RESULT 12

US-09-745-842-4  
 ; Sequence 4, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: F2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 4  
 ; LENGTH: 315  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-745-842-4

Query Match 91.9%; Score 1634; DB 12; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 2.5e-145;  
 Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MOAVDNLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
 Db 1 MOAVDNLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLTTPFPKILSDAKLTGTPRTFVCQVTSVIFFTMYISISFLGLITI 120  
 Db 61 IFLKNTVISDLMLTTPFPKILSDAKLTGTPRTFVCQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTRPPTSPKPNLLGAKILSVIWAFFMLSLPNMILTNQPRDKNVKKSFLKS 180  
 Db 121 DRYQKTRPPTSPKPNLLGAKILSVIWAFFMLSLPNMILTNQPRDKNVKKSFLKS 180  
 QY 181 BFLGVWHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVGVPRKKNVKVFI 240  
 Db 181 BFLGVWHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVGVPRKKNVKVFI 240  
 QY 241 IIAVFFICFVPHFARIPTLTSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFF 300  
 Db 241 IIAVFFICFVPHFARIPTLTSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFF 300  
 QY 301 LCKSPRNSLSMLKC 315  
 Db 301 LCKSPRNSLSMLKC 315

RESULT 13

US-09-745-842-2  
 ; Sequence 2, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: P2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26

; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2  
 ; LENGTH: 343  
 ; TYPE: PRT  
 ; ORGANISM: Rattus norvegicus  
 US-09-745-842-2  
 Query Match 86.0%; Score 1528.5; DB 12; Length 343;  
 Best Local Similarity 86.9%; Pred. No. 2.2e-135;  
 Matches 293; Conservative 17; Mismatches 22; Indels 5; Gaps 1;  
 QY 6 NLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIILKN 65  
 Db 12 NLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFIILKN 71  
 QY 66 TVISDLMLTTPFPKILSDAKLTGTPRTFVCQVTSVIFFTMYISISFLGLITIDRYK 125  
 Db 72 TVISDLMLTTPFPKILSDAKLTGTPRTFVCQVTSVIFFTMYISISFLGLITIDRYK 131  
 QY 126 TTRPPTSPKPNLLGAKILSVIWAFFMLSLPNMILTNQPRDKNVKKSFLKSEGLV 185  
 Db 132 TTRPPTSPKPNLLGAKILSVIWAFFMLSLPNMILTNQPRDKNVKKSFLKSEGLV 191  
 QY 186 WHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVGVPRKKNVKVFIILAVF 245  
 Db 192 WHEIVNYICQVIFWIFNLIVCYTLITKELYRSYVTRGVGVPRKKNVKVFIILAVF 251  
 QY 246 FICFVPHFARIPTLTSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFLCKSF 305  
 Db 252 FICFVPHFARIPTLTSQTRDVEDCTAENTLFYVKESTLWLSNACLDPPFIYFLCKSF 311  
 QY 306 RNSLSMLKCPNSATSQSDNRKKBQDGGDPNEETPM 342  
 Db 312 RNSLSMLKCPNSATSQSDNRKKBQDGGDPNEETPM 343

RESULT 14

US-09-745-842-12  
 ; Sequence 12, Application US/09745842  
 ; Publication No. US2003017077A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conley, Pamela B.  
 ; APPLICANT: Jantzen, Hans-Michael  
 ; APPLICANT: Ramakrishnan-Dubridge, Vanitha  
 ; APPLICANT: Julius, David  
 ; APPLICANT: Hollopeter, Gunter  
 ; APPLICANT: COR Therapeutics, Inc.  
 ; TITLE OF INVENTION: P2Y12 Receptor  
 ; FILE REFERENCE: 44481-5053-US  
 ; CURRENT APPLICATION NUMBER: US/09/745,842  
 ; CURRENT FILING DATE: 2000-12-26  
 ; PRIOR APPLICATION NUMBER: US 60/171,622  
 ; PRIOR FILING DATE: 1999-12-23  
 ; NUMBER OF SEQ ID NOS: 21  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 267  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-745-842-12  
 Query Match 69.6%; Score 1237.5; DB 12; Length 267;  
 Best Local Similarity 95.7%; Pred. No. 3.5e-108;  
 Matches 242; Conservative 3; Mismatches 7; Indels 1; Gaps 1;  
 QY 1 MOAVDNLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
 Db 1 MOAVDNLTSAAGNTSLCTRDYKTIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLTTPFPKILSDAKLTGTPRTFVCQVTSVIFFTMYISISFLGLITI 120

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Db 61 IFLKNTVISDLLMILTFPFKILSDAKLGTGLRTFVCQVTSVIFYFTMYISFLGLITI 120
Qy 121 DRYOKTRPRKTSNPKNLLGAKILSVVIAFMFLLSPNNMILNROPRDRKNVKKCSFLKS 180
Db 121 DRYOKTRPRKTSNPKNLLGAKILSVVIAFMFLLSPNNMILNROPRDRKNVKKCSFLKS 180
Qy 181 EFGVLWHEIVNYICQVIFWNLFLIVCYTLITKELYRSVVRTRGVGVPRKKVNVKVF 240
Db 181 EFGVLWHEIVNYICQVIFWNLFLIVCYTLITKELYRSVVRTRGVGVPRKKVNVKVF 240
Qy 241 IIAVFPI-CFVPF 252
Db 241 HCCILYLFCSPPF 253
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## RESULT 15

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US-09-924-125-2
; Sequence 2, Application US/09924125
; Publication No. US20030050235A1
; GENERAL INFORMATION:
; APPLICANT: Communi, Didier
; TITLE OF INVENTION: THE NATURAL LIGAND FOR ORPHAN G PROTEIN COUPLED RECEPTOR GPR86 AN
; FILE REFERENCE: 9049/2092
; CURRENT APPLICATION NUMBER: US/09/924,125
; CURRENT FILING DATE: 2001-07-08
; PRIOR APPLICATION NUMBER: US 09/924,125
; PRIOR FILING DATE: 2001-07-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-924-125-2
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Query Match 46.6%; Score 829; DB 11; Length 333;
Best Local Similarity 49.1%; Pred.No.1.le-69;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

Qy 17 CTRDYKITQVLPPLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFLKNVTISDLMILT 76
Db 15 CPRDTRIVQLVFPALYTVVFLTGILLNTLALWVFIIPSSSTFIYLYKNTLVADLIMTLM 74
Qy 77 FPFKILSDAKLGTGLRTFVCQVTSVIFYFTMYISFLGLITIDRYOKTRPRKTSNEK 136
Db 75 LPFKILSDSHLAPQLRAFVCRFSSVIFYETMYVGVILLGLIAFDRFLKIIRPLRNIFLK 134
Qy 137 NLLGAKILSVVIAFMFLLSPNNMILNROPRDRKNVKKCSFLKSEFGLVWHEIVNYICQV 196
Db 135 KPVEAKTVSIFINWFFLFIISLPNNILSNKEATPSSVKKCSLGLKGLKHQWNNICQF 194
Qy 197 IFWNLFLIVCYTLITKELYRSVVRTRGVGVPRKKVNVKVFIIIAVFPICFVPFHPAR 256
Db 195 IFWTVFIMLVFYVVIARVYDYSRKSKDRKNKKGKGVVAVFVCFVCFAPFHPAR 254
Qy 257 IPYTLSTORVDFDCTAENTLFFYKVESTLWLTSLNACLDPFIYFPFLCKSPNSLSMLKCP 316
Db 255 VPYTHSQTNKTKDRLQNLQFIKAKETTLFLAATNICMDPLIYIPLCKTEKLPCCNQ--G 312
Qy 317 NSATSLSQDNKKKEQD 332
Db 313 RKTASSQENHSSQTD 328
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Search completed: February 4, 2004, 14:28:07  
Job time : 38 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 4, 2004, 14:23:06 ; Search time 43 Seconds  
(without alignments)  
1262.430 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKKEQGGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
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- 22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*
- 24: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1778	100.0	342	20	AAW81576
2	1778	100.0	342	21	AAW81576
3	1778	100.0	342	21	AAW81576
4	1778	100.0	342	21	AAW81576
5	1778	100.0	342	22	AAW81576
6	1778	100.0	342	22	AAW81576
7	1778	100.0	342	23	AAW81576
8	1778	100.0	342	23	AAW81576
9	1778	100.0	342	23	AAW81576

10	1778	100.0	342	23	AAW81576	Human G protein-co
11	1778	100.0	342	23	AAW81576	Human SP168 recept
12	1778	100.0	342	23	AAW81576	Human PAFR3 protei
13	1778	100.0	342	24	AAW81576	Human P212 platele
14	1748	98.3	342	21	AAW81576	Macaque ortholog o
15	1634	91.9	315	22	AAW81576	Murine P2-purinerg
16	1555.5	87.5	347	23	AAW81576	Murine G protein-c
17	1528.5	86.0	343	22	AAW81576	Rat P2-purinergic
18	1493.5	84.0	387	21	AAW81576	Rat MP-10 receptor
19	1237.5	69.6	267	22	AAW81576	Human P2-purinerg
20	829	46.6	333	21	AAW81576	Human chemokine re
21	829	46.6	333	22	AAW81576	Human G protein co
22	829	46.6	333	22	AAW81576	Novel human G prot
23	829	46.6	333	24	AAW81576	G protein-coupled
24	827	46.5	333	22	AAW81576	Human CON203 G pro
25	823	46.3	333	20	AAW81576	Human 7-transmembr
26	823	46.3	333	20	AAW81576	Human orphan G pro
27	823	46.3	333	21	AAW81576	Human G protein co
28	823	46.3	333	22	AAW81576	Human HNEA481 poly
29	823	46.3	333	22	AAW81576	Amino acid sequenc
30	823	46.3	333	23	AAW81576	Human GPCR polypep
31	810.5	45.6	336	22	AAW81576	Rat 7-transmembran
32	797	44.8	333	19	AAW81576	Human chemokine re
33	797	44.8	333	23	AAW81576	Chemokine receptor
34	792	44.5	337	22	AAW81576	Mouse G protein-co
35	772	43.4	338	21	AAW81576	Human UDP-glucose
36	772	43.4	338	22	AAW81576	Human stem cell G-
37	772	43.4	338	23	AAW81576	Human endometrial
38	772	43.4	338	24	AAW81576	Human UDP-glucose
39	772	43.4	338	24	AAW81576	Rat KIAA0001 prote
40	769	43.3	338	21	AAW81576	Mouse 7-transmembr
41	741.5	41.7	338	21	AAW81576	Mouse stem cell G-
42	741.5	41.7	338	23	AAW81576	Mouse EBV-induced
43	725	40.8	166	22	AAW81576	Human protein SEQ
44	725	40.8	166	22	AAW81576	Human protein sequ
45	699.5	39.3	358	22	AAW81576	

## ALIGNMENTS

RESULT 1	AAW81576	AAW81576 standard; Protein; 342 AA.
ID	AAW81576	standard; Protein; 342 AA.
XX	AAW81576;	
AC	AAW81576;	
XX	AAW81576;	
DT	22-FEB-1999	(first entry)
XX	22-FEB-1999	(first entry)
DE	EBV-induced G-protein coupled receptor (EBI-2) polypeptide.	
XX	EBV-induced G-protein coupled receptor; EBI-2; Epstein-Barr Virus; ulcer;	
KW	endothelium-differentiation gene; EDG-1-like G-protein coupled receptor;	
KW	recombinant; agonist; asthma; Parkinson's disease; heart failure; asthma;	
KW	hypertension; urinary retention; osteoporosis; antagonist; hypertension;	
KW	angina pectoris; myocardial infarction; allergy; psychosis; depression;	
KW	migraine; vomiting; stroke; eating disorder; migraine headache; cancer;	
KW	prostatic hypertrophy; detection; drug screening.	
OS	Homo sapiens.	
XX	Homo sapiens.	
FT	Key	Location/Qualifiers
FT	Misc-difference 6	/note= "encoded by ATT"
FT	Misc-difference 14	/note= "encoded by AAC"
XX	WO9805049-A2.	
PN	WO9805049-A2.	
XX	12-NOV-1998.	
PD	12-NOV-1998.	
XX	07-MAY-1998;	98WO-US09048.
PF	07-MAY-1998;	98WO-US09048.
XX	07-MAY-1998;	98WO-US09048.

PR 07-MAY-1997; 97US-0852824.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Li Y, Ruben SM;  
 XX WPI; 1999-034722/03.  
 DR N-PSDB; AAV69760.  
 XX New isolated human G-protein coupled receptors - used to develop  
 PT products for treating e.g. asthma, Parkinson's disease, heart  
 PT failure, osteoporosis, hypertension, psychoses, eating disorders or  
 PT cancers  
 XX Claim 1; Fig 1A-C; 65pp; English.  
 PS This represents a EBV-induced G-protein coupled receptor (EBI-2)  
 XX polypeptide. The encoding DNA is deposited under the accession number  
 CC ATCC No: 209003. The invention provides two human G-protein coupled  
 CC receptor polypeptides. The polypeptides are human Epstein-Barr Virus  
 CC (EBV)-induced G-protein coupled receptor, designated EBI-2 polypeptide  
 CC and a human endothelium-differentiation gene (EDG) like G-protein coupled  
 CC receptor, designated EDG-1-like G-protein coupled receptor. Vectors  
 CC comprising the EBI-2 and EDG-1-like polypeptides encoding DNA can be used  
 CC to transform host cells for the recombinant production of the proteins.  
 CC Agonists for G-protein coupled receptors can be used for the treatment of  
 CC asthma, Parkinson's disease, acute heart failure, hypotension, urinary  
 CC retention and osteoporosis. Antagonists can be used for the treatment of  
 CC hypertension, angina pectoris, myocardial infarction, ulcers, asthma,  
 CC allergies, psychoses, depression, migraine, vomiting, stroke, eating  
 CC disorders, migraine headaches, cancer and benign prostatic hypertrophy.  
 CC The products can also be used for detection, diagnosis and drug  
 CC screening.  
 XX Sequence 342 AA;  
 SQ

Query Match 100.0%; Score 1778; DB 20; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQAVNLTSAPOGNTSLCTRDYKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60  
 Db 1 MQAVNLTSAPOGNTSLCTRDYKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60  
 QY 61 IFKNTVLSLMLITFPFKILSDAKLGTGPIRTFVCQVTSVIFFTMYISIFGLITI 120  
 Db 61 IFKNTVLSLMLITFPFKILSDAKLGTGPIRTFVCQVTSVIFFTMYISIFGLITI 120  
 QY 121 DRYQKTRFETKSNPKNLGAKILSVIWAFFLLSLNMLITNRPDKNVKCSFLKS 180  
 Db 121 DRYQKTRFETKSNPKNLGAKILSVIWAFFLLSLNMLITNRPDKNVKCSFLKS 180  
 QY 181 EFLGVNHEIVNYICQVIFWFINFLIVICVTLITKELYSYVTRGVKVPKKNVNVFI 240  
 Db 181 EFLGVNHEIVNYICQVIFWFINFLIVICVTLITKELYSYVTRGVKVPKKNVNVFI 240  
 QY 241 IIAVFFICVPFHARIPVTLSTQDRVDFCTAENTLFVVKESTLWLTSLNACLDPFIYFF 300  
 Db 241 IIAVFFICVPFHARIPVTLSTQDRVDFCTAENTLFVVKESTLWLTSLNACLDPFIYFF 300  
 QY 301 LCKSFNSLSMLKCPNSATSLSQDNRRKKEQDGPNEETPM 342  
 Db 301 LCKSFNSLSMLKCPNSATSLSQDNRRKKEQDGPNEETPM 342

RESULT 2

AA71306

ID AAY71306 standard; Protein; 342 AA.

XX AAY71306;

DT 02-NOV-2000 (first entry)

XX

DE Human orphan G protein-coupled receptor hCHN8.  
 XX Human; orphan G protein-coupled receptor; GPCR; hCHN8; drug screening;  
 KW transmembrane receptor; expressed sequence tag; EST; signal cascade.  
 KW Homo sapiens.  
 OS WO2000031258-A2.  
 XX 02-JUN-2000.  
 PD 13-OCT-1999; 99WO-US23687.  
 PF 20-NOV-1998; 98US-0109213.  
 PR 16-FEB-1999; 98US-0120415.  
 PR 26-FEB-1999; 98US-0121852.  
 PR 12-MAR-1999; 99US-0123946.  
 PR 12-MAR-1999; 99US-0123949.  
 PR 28-MAY-1999; 98US-0136436.  
 PR 28-MAY-1999; 98US-0136437.  
 PR 28-MAY-1999; 98US-0136439.  
 PR 28-MAY-1999; 98US-0136567.  
 PR 28-MAY-1999; 98US-0137127.  
 PR 28-MAY-1999; 98US-0137131.  
 PR 29-JUN-1999; 98US-0141448.  
 PR 29-SEP-1999; 98US-0156555.  
 PR 29-SEP-1999; 98US-0156633.  
 PR 29-SEP-1999; 98US-0156634.  
 PR 01-OCT-1999; 98US-0157280.  
 PR 01-OCT-1999; 98US-0157281.  
 PR 01-OCT-1999; 98US-0157282.  
 PR 01-OCT-1999; 98US-0157293.  
 PR 01-OCT-1999; 98US-0157294.  
 PR 12-OCT-1999; 98US-0416760.  
 PR 12-OCT-1999; 98US-0417044.  
 XX (AREN-) ARENA PHARM INC.  
 PA Chen R, Dang HT, Liaw CW, Lin I;  
 PI WPI; 2000-400068/34.  
 DR N-PSDB; AAD01133.  
 XX Novel human orphan G protein-coupled receptors and the encoding cDNAs  
 PT for use in the identification of G protein-coupled receptor agonists -  
 PS Claim 62; Page 82-83; 102pp; English.  
 XX The present amino acid sequence is the hCHN8, an endogenous human  
 CC orphan G protein-coupled receptor (GPCR), expressed in left and right  
 CC cerebellum, kidney and lung. The hCHN8 cDNA was identified using full  
 CC length EST (expressed sequence tag) 764455 as a probe.  
 CC The orphan GPCR of the invention, like all GPCRs has seven transmembrane  
 CC alpha helices with an extracellular N-terminus and an intracellular  
 CC C-terminus. However, no endogenous ligands has yet been identified for  
 CC the proteins of the invention. The orphan GPCRs may be used in the  
 CC identification of their endogenous ligands, and to screen potential GPCR  
 CC agonists and antagonists for use as pharmaceutical agents. The proteins  
 CC may also be used in the study of GPCR-mediated signalling cascades, and  
 CC to elucidate their precise role in normal and diseased human conditions.  
 CC Nucleic acid encoding human orphan GPCRs may be used for tissue  
 CC localisation expression analysis to provide information about their  
 CC function in healthy and pathological states.  
 XX Sequence 342 AA;  
 SQ

Query Match 100.0%; Score 1778; DB 21; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSAPOGNTSLCTRDYKITQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60

Db 1 MQAVDNLTSAAGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVVWAFMFLSLPNMILTNQPRDKNVKCSFLKS 180  
Db 121 DRYQKTRPPKTSNPKNLLGAKILSVVWAFMFLSLPNMILTNQPRDKNVKCSFLKS 180  
QY 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSVYRTRGVGKVPKKNVKVFI 240  
Db 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSVYRTRGVGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHPIRYTLSTQTRDVFDCVTAENTLIFYVKESTLWLTSLNACLDPPFIYFF 300  
Db 241 IIAVFFICFVFPFHPIRYTLSTQTRDVFDCVTAENTLIFYVKESTLWLTSLNACLDPPFIYFF 300  
QY 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
Db 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 3  
AAB02840  
ID AAB02840 standard; Protein; 342 AA.  
XX AAB02840;  
AC AAB02840;  
DT 22-AUG-2000 (first entry)  
TX Human G protein coupled receptor hCHN8 protein SEQ ID NO:34.  
DE Human; G protein coupled receptor; GPCR; transmembrane receptor;  
KW identification; agonist; screening; therapeutic; pharmaceutical;  
KW mutant.  
XX Homo sapiens.  
OS Homo sapiens.  
PN W0200022131-A2.  
EN 20-APR-2000.  
PD 20-APR-2000.  
XX 13-OCT-1999; 99WO-US24065.  
PF 13-OCT-1998; 98US-0170496.  
PR 12-NOV-1998; 98US-0108029.  
PR 20-NOV-1998; 98US-0109213.  
PR 27-NOV-1998; 98US-0110060.  
PR 16-FEB-1999; 99US-0120416.  
PR 26-FEB-1999; 99US-0121852.  
PR 12-MAR-1999; 99US-0123944.  
PR 12-MAR-1999; 99US-0123945.  
PR 12-MAR-1999; 99US-0123946.  
PR 12-MAR-1999; 99US-0123948.  
PR 12-MAR-1999; 99US-0123949.  
PR 12-MAR-1999; 99US-0123951.  
PR 28-MAY-1999; 99US-0136436.  
PR 28-MAY-1999; 99US-0136437.  
PR 28-MAY-1999; 99US-0136439.  
PR 28-MAY-1999; 99US-0137127.  
PR 28-MAY-1999; 99US-0137131.  
PR 28-MAY-1999; 99US-0137567.  
PR 30-JUN-1999; 99US-0141448.  
PR 27-AUG-1999; 99US-0151114.  
PR 03-SEP-1999; 99US-0152524.  
PR 29-SEP-1999; 99US-0156633.  
PR 29-SEP-1999; 99US-0156555.  
PR 29-SEP-1999; 99US-0156634.  
XX (AREN-) ARENA PHARM INC.  
PA Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;  
XX WPI; 2000-317986/27.  
DR N-ESDB; AAA46034.  
XX Non-endogenous, human G protein-coupled receptors for screening  
PT receptor, inverse or partial agonists useful as therapeutic agents -  
XX Example 1; Page 112-113; 187pp; English.  
XX The present invention describes transmembrane receptors, preferably  
CC human G protein coupled receptors (GPCR), for which the endogenous  
CC ligand is unknown (orphan GPCR receptors). More specifically the present  
CC invention relates to non-endogenous, constitutively activated versions  
CC of a human GPCR. These non-endogenous human GPCRs can be useful for  
CC the direct identification of candidate compounds as receptors agonists,  
CC inverse agonists or partial agonists for use as pharmaceutical agents.  
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in  
CC the exemplification of the present invention.  
XX Sequence 342 AA;  
SQ Query Match 100.0%; Score 1778; DB 21; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MQAVDNLTSAAGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
Db 1 MQAVDNLTSAAGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFQIRSKSNFI 60  
QY 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
Db 61 IFLKNTVISDLLMILTPFPKILSDAKLGTGTLRTFVCQVTSVIFFTMYISISFLGLITI 120  
QY 121 DRYQKTRPPKTSNPKNLLGAKILSVVWAFMFLSLPNMILTNQPRDKNVKCSFLKS 180  
Db 121 DRYQKTRPPKTSNPKNLLGAKILSVVWAFMFLSLPNMILTNQPRDKNVKCSFLKS 180  
QY 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSVYRTRGVGKVPKKNVKVFI 240  
Db 181 EFGLVWHEIYVNYICQVIFWNLFLIVCYTLITKELYRSVYRTRGVGKVPKKNVKVFI 240  
QY 241 IIAVFFICFVFPFHPIRYTLSTQTRDVFDCVTAENTLIFYVKESTLWLTSLNACLDPPFIYFF 300  
Db 241 IIAVFFICFVFPFHPIRYTLSTQTRDVFDCVTAENTLIFYVKESTLWLTSLNACLDPPFIYFF 300  
QY 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342  
Db 301 LCKSFRNSLSMLKCPNSATSLSDNRKKEQDGDGDPNEETPM 342

RESULT 4  
AAY94444  
ID AAY94444 standard; protein; 342 AA.  
XX AAY94444;  
AC AAY94444;  
XX 21-AUG-2000 (first entry)  
DT Human 15625 receptor protein.  
TX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;  
KW Gliol cells; spleen; colon; liver; brain; T-cell; heart; 3;  
KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;  
KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
FH Key Location/Qualifiers  
FT Domain 1..25  
FT Modified-site /label= extracellular\_domain  
FT /label= N-glycosylation





RESULT 7  
ABP95608  
ID ABP95608 standard; Protein, 342 AA.

AC ABP95608;  
DT 06-MAR-2003 (first entry)  
XX

DE Human GPCR polypeptide SEQ ID NO 26.

XX Human; GPCR; G protein coupled receptor; signal transduction; olfactory;  
KW drug development; gustatory; taste; fragrance; receptor.  
XX

OS Homo sapiens.

PN WO200216548-A2.

XX 28-FEB-2002.

XX 30-JUL-2001; 2001WO-IB01446.

XX 04-AUG-2000; 2000JP-0237818.

XX 13-FEB-2001; 2001JP-0034434.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.

XX Haga T, Takeda S, Mitaku S;

XX WPI; 2002-304118/34.

XX N-PSDB; ABZ42882.

XX Database global search for G protein-coupled receptors, proteins and  
PT encoded genes for studying in vivo signal transduction mechanism and  
PT identifying targets for drug development

XX Claim 10; SEQ ID NO 26; 97pp + Sequence Listing; Japanese.

XX The invention relates to a method for screening G protein-coupled  
CC receptor (GPCR) genes (ABZ42870-ABZ43216) and/or GPCR proteins  
CC (ABP95596-ABP95942) by extracting open-reading frames containing 6-8  
CC transmembrane domains with 250-1000 amino acid residues to give a gene  
CC homologous with a known GPCR gene. The receptor proteins and encoded  
CC genes are useful for studying in vivo signal transduction mechanism and  
CC identifying targets for drug development e.g. based on olfactory and  
CC gustatory receptors in form of agonists and antagonists by screening  
CC intrinsic and extrinsic ligands as bitter taste inhibitors, taste  
CC enhancers and fragrance improvers.

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 23; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTAPGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60

DB 1 MQAVNLTAPGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60

QY 61 IFKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120

DB 61 IFKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKNVKCSFLKS 180

DB 121 DRYQKTRTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKNVKCSFLKS 180

QY 181 EFLGVWHEIVNVIQVIFWFINFLIVVCTLTITKELYSYVTRGVGKVPKKNVNVKFI 240

DB 181 EFLGVWHEIVNVIQVIFWFINFLIVVCTLTITKELYSYVTRGVGKVPKKNVNVKFI 240

QY 241 IIAVFFICFVFFHARIPYTLISQTRDVFDCVTAENTLFVKESTLWLTSLNACLDPFIYFF 300  
DB 241 IIAVFFICFVFFHARIPYTLISQTRDVFDCVTAENTLFVKESTLWLTSLNACLDPFIYFF 300  
QY 301 LCKSPNLSLMLKCPNSATSLSQNRKKEQDGGDPNEETPM 342  
DB 301 LCKSPNLSLMLKCPNSATSLSQNRKKEQDGGDPNEETPM 342

RESULT 8

ABB77868  
ID ABB77868 standard; Protein, 342 AA.

XX ABB77868;

XX 27-SEP-2002 (first entry)

XX Amino acid sequence of human ADP receptor P2TAC protein.

XX Human; ADP receptor; P2TAC; antiplatelet agent; thrombotic disease;  
KW ischaemic disease.

XX Homo sapiens.

XX WO200236631-A1.

XX 10-MAY-2002.

XX 31-OCT-2001; 2001WO-JP09534.

XX 01-NOV-2000; 2000JP-0334721.

XX 11-JAN-2001; 2001JP-0003577.

XX (YAMA) YAMANOUCHI PHARM CO LTD.

XX Takasaki J, Matsumoto M, Kamohara M, Saito T, Ohishi T, Soga T;

XX WPI; 2002-519236/55.

XX N-PSDB; ABL59205.

XX Method for screening anti-platelet agents with human ADP receptor P2TAC  
PT protein, its functional equivalent, or its homologous protein, as tool,  
PT for treating e.g. thrombotic or ischaemic diseases

XX Claim 1; Page 48-49; 56pp; Japanese.

XX The present sequence represents a human ADP receptor P2TAC protein. It is  
CC used as a screening tool for screening for antiplatelet agents. The  
CC method is used for screening for antiplatelet agents, which can then  
CC be used for treating e.g. thrombotic or ischaemic diseases.

XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 23; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTAPGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60

DB 1 MQAVNLTAPGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRKSNFI 60

QY 61 IFKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120

DB 61 IFKNTVISDLMLITFPFKILSDAKLGTGRLTFVCOVTSVIFFTMYISISFLGLITI 120

QY 121 DRYQKTRTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKNVKCSFLKS 180

DB 121 DRYQKTRTRPFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNRPQDKNVKCSFLKS 180

QY 181 EFLGVWHEIVNVIQVIFWFINFLIVVCTLTITKELYSYVTRGVGKVPKKNVNVKFI 240

DB 181 EFLGVWHEIVNVIQVIFWFINFLIVVCTLTITKELYSYVTRGVGKVPKKNVNVKFI 240

QY 241 IIAVFFICFVPPHFAPIPTLSTQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
DB 241 IIAVFFICFVPPHFAPIPTLSTQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
QY 301 LCKSPRNSLSMLKCPNSATSLSDNRKKKGQGGDPNEETPM 342  
DB 301 LCKSPRNSLSMLKCPNSATSLSDNRKKKGQGGDPNEETPM 342  
RESULT 9  
AAU80164  
ID AAU80164 standard; Protein; 342 AA.  
XX AAU80164;  
XX  
DT 15-JUL-2002 (first entry)  
XX  
DE Human ADP-glucose receptor.  
XX  
KW Human; ADP-glucose; receptor; G protein-coupled receptor;  
KW agonist; antagonist; cardiovascular function disorder; vasorelaxation;  
KW ischaemia; angina pectoris; gastrointestinal disorder; diarrhoea;  
KW immune disorder; immunodeficiency disorder; autoimmune disorder;  
KW rheumatoid arthritis; bacterial infection; viral infection;  
KW fungal infection; protozoal infection; respiratory disorder; asthma;  
KW kidney disorder; glomerulonephritis; hepatobiliary disorder; cirrhosis;  
KW endocrine disorder; adrenal dysfunction; musculoskeletal disorder;  
KW osteoporosis; nervous system disorder; Alzheimer's disease;  
KW psychotic disorder; depression; cancer; pain; glycogen storage disease;  
KW disorder of body weight; AIDS; acquired immunodeficiency syndrome;  
KW chromosome 3; Usher's syndrome type 3.  
XX  
OS Homo sapiens.  
XX  
FN WO200224942-A2.  
XX  
PD 28-MAR-2002.  
XX  
PF 19-SEP-2001; 2001WO-US29523.  
XX  
PR 20-SEP-2000; 2000US-234025P.  
PR 09-FEB-2001; 2001US-0780576.  
XX  
XX (REGC ) UNIV CALIFORNIA.  
XX  
XX Civelli O, Nothacker H, Wang Z, Reinscheid R;  
XX  
XX WPI, 2002-383195/41.  
XX N-PSDB; ABK50286.  
XX  
PT Identifying an agonist, antagonist or ligand of an ADP-glucose  
PT receptor, for treating cardiovascular, gastrointestinal, kidney,  
PT endocrine, immune disorders, and bacterial, viral, protozoal or fungal  
PT infections  
XX  
PS Claim 3; Fig 1; 86pp; English.

The ant/agonists are useful therapeutically for preventing or ameliorating conditions associated with the receptor such as cardiovascular disorders (e.g. ischaemia, hypertension, hypotension, angina pectoris, myocardial infarction, stroke, congestive heart failure, shock, erectile dysfunction, orthostatic intolerance and migraine), gastrointestinal disorders (e.g. diarrhoea, gastritis, inflammatory bowel disease), immune disorders (e.g. immunodeficiency disorders, autoimmune disorders, rheumatoid arthritis), infections caused by bacteria, fungi, protozoa or virus, respiratory disorders (e.g. asthma, pneumonia, bronchitis), kidney disorders (e.g. glomerulonephritis, renal failure, lupus), hepatobiliary disorders (e.g. jaundice, cirrhosis, hepatitis), endocrine disorders (e.g. pituitary, thyroid or adrenal dysfunctions), musculoskeletal disorders (e.g. osteoporosis, muscular dystrophies), nervous system disorders (e.g. Parkinson's and Alzheimer's disease), pain, glycogen storage depression, anxiety, schizophrenia), pain, glycogen storage depression, anxiety, schizophrenia). The gene for the ADP-G or AIDS, acquired immunodeficiency syndrome). The gene for the ADP-G receptor is located on chromosome 3 in a region associated with Usher syndrome type 3 (progressive hearing loss). The ligand is useful therapeutically, in detecting normal or abnormal expression of the receptor in an isolated sample or in vivo diagnostic imaging procedures, and targeting specifically a diagnostic group to cells and tissues that express the receptor. The present sequence represents the ADP-G receptor.

Query Match 100.0%; Score 1778; DB 23; Length 342;  
Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTYLVFFVGLITNGLAMRIFPQIRSKNFI 60  
DB 1 MOAVDNLTSAPGNTSLCTRDYKIKITQVLPFLLYTYLVFFVGLITNGLAMRIFPQIRSKNFI 60  
QY 61 IFLKNTVISDLLMLTTPFPKILSDAKLGTGPRFVQCVTSVIFFTYISIFGLITI 120  
DB 61 IFLKNTVISDLLMLTTPFPKILSDAKLGTGPRFVQCVTSVIFFTYISIFGLITI 120  
QY 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAQFVLLSLPNMILTNRQPKDNKVKCSFLKS 180  
DB 121 DRYQKTRTPFKTSNPKNLLGAKILSVIWAQFVLLSLPNMILTNRQPKDNKVKCSFLKS 180  
QY 181 EFLVWHEIVNYICQVIFWIFNLIVVYITLITKELVRSYVTRTGKVPKKNVNVKFI 240  
DB 181 EFLVWHEIVNYICQVIFWIFNLIVVYITLITKELVRSYVTRTGKVPKKNVNVKFI 240  
QY 241 IIAVFFICFVPPHFAPIPTLSTQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
DB 241 IIAVFFICFVPPHFAPIPTLSTQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
QY 301 LCKSPRNSLSMLKCPNSATSLSDNRKKKGQGGDPNEETPM 342  
DB 301 LCKSPRNSLSMLKCPNSATSLSDNRKKKGQGGDPNEETPM 342

RESULT 10  
AAU48353  
ID AAU48353 standard; Protein; 342 AA.  
XX  
XX AAU48353;  
XX  
DT 25-APR-2002 (first entry)  
XX  
DE Human G protein-coupled receptor, IGPCRI7.  
XX  
KW Human; G protein-coupled receptor; IGPCRI7; analgesic; neuroleptic;  
KW tranquilizer; antiparkinsonian; neuroprotective; nootropic;  
KW anticonvulsant; metabolic; anorectic; anabolic; antiinflammatory;  
KW antidiarrheic; osteopathic; antistomatitic; antiallergic; antiarthritic;  
KW immunosuppressive; gene therapy; psychiatric disorder; schizophrenia;  
KW central nervous system disorder; movement dysfunction; schizophrenia;

KW multiple sclerosis; Alzheimer's disease; kidney disease; obesity;  
 KW gastrointestinal disorder; osteoporosis; infection;  
 KW gynecological disorder; receptor.  
 XX Homo sapiens.  
 OS  
 FN WO200202599-A2.  
 XX  
 PD 10-JAN-2002.  
 XX  
 PF 02-JUL-2001; 2001WO-EP07532.  
 XX  
 PR 30-JUN-2000; 2000US-215759P.  
 XX  
 PA (INGE-) INGENIUM PHARM AG.  
 XX  
 PI Wattler F, Wattler S, Trommler P, Nehls MC;  
 XX  
 DR WPI: 2002-140080/18.  
 DR N-PSDB; ABA98535.  
 XX  
 PT New human or mouse G protein-coupled receptor protein, IGPCR17, useful  
 PT for diagnosis, prevention, amelioration or treatment of central nervous  
 PT system disorders such as Tourette's syndrome, Parkinson's disease and  
 PT pain.  
 XX  
 PS Claim 8; Fig 2; 71pp; English.  
 XX  
 CC The present sequence is the protein sequence for human G protein-coupled  
 CC receptor (GPCR) protein, IGPCR17. The coding sequence for IGPCR17 is  
 CC useful in gene therapy for prevention, amelioration or treatment of  
 CC diseases characterised by aberrant expression or activity of IGPCR17,  
 CC where the disease is a psychiatric or central nervous system (CNS)  
 CC disorder associated with signal processing in CNS such as learning and  
 CC memory disorders, movement dysfunctions, tics, tremor, Tourette's  
 CC syndrome, Parkinson's disease, Huntington's disease, dyskinesias,  
 CC dystonia, pain and spasms. In addition, IGPCR17 and its coding sequence  
 CC are useful in diagnosis, prevention, amelioration or treatment of  
 CC diseases associated with signal processing in CNS, schizophrenia,  
 CC episodic paroxysmal anxiety (EPA) disorders such as obsessive compulsive  
 CC disorder (OCD), multiple sclerosis, Alzheimer's disease/dementia,  
 CC anorexia, kidney diseases such as renal failure, obesity,  
 CC gastrointestinal disorders such as irritable bowel syndrome (IBS),  
 CC diarrhoea, motility disorders and conditions of delayed gastric emptying,  
 CC osteoporosis, infections such as bacterial, fungal, protozoal and viral  
 CC infections, asthma, allergy, arthritis, sepsis and gynecological  
 CC disorders.  
 XX  
 SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5,3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQAVDNLTSAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFQIRSKNFI 60  
 DB 1 MQAVDNLTSAPGNTSLCTRDYKITQVLPFLTYVLFVGLITNGLAMRIFQIRSKNFI 60  
 QY 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFCQVTSVIFFTWYISIFGLITI 120  
 DB 61 IFLKNTVISDLMLITFPFKILSDAKLGTGRLTFCQVTSVIFFTWYISIFGLITI 120  
 QY 121 DRYQKTRFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNQPRDKNVKCSFLKS 180  
 DB 121 DRYQKTRFKTSNPKNLGAKILSVIWAFFLLSLPNMILTNQPRDKNVKCSFLKS 180  
 QY 181 EFLVWHEIVNYICQVIFWIFNLIVICVYTLTKELYSYVTRGVGKPRKKNVKVI 240  
 DB 181 EFLVWHEIVNYICQVIFWIFNLIVICVYTLTKELYSYVTRGVGKPRKKNVKVI 240  
 QY 241 IIAVFFICVDFHFAIPVTLSTQTRVDFCTAENTLFYVKESTLMTLSNACLDPIYFF 300  
 DB 241 IIAVFFICVDFHFAIPVTLSTQTRVDFCTAENTLFYVKESTLMTLSNACLDPIYFF 300

QY 301 LCKSPRNSLMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342  
 DB 301 LCKSPRNSLMLKCPNSATSLSDNRKKEQDGGDPNEETPM 342

RESULT 11  
 ID ABB05031  
 XX ABB05031 standard; Protein; 342 AA.  
 AC ABB05031;  
 XX  
 DT 25-MAR-2002 (first entry)  
 XX  
 DE Human SP168 receptor protein SEQ ID NO:2.  
 XX

KW Human; SP168 receptor; mammalian G-Protein coupled receptor; GPCR;  
 KW neurodegenerative disorder; Parkinson's disease; Alzheimer's disease;  
 KW Huntington's disease; amyotrophic lateral sclerosis; ALS; MS; receptor;  
 KW multiple sclerosis.  
 XX

OS Homo sapiens.  
 XX  
 FN US2001046497-A1.  
 XX  
 PD 29-NOV-2001.  
 XX  
 PF 16-APR-2001; 2001US-0835922.  
 XX  
 PR 21-APR-2000; 2000US-199041P.  
 XX

(ZHAN/) ZHANG F L.  
 (LUOL/) LUO L.  
 (GUST/) GUSTAFSON E.  
 (LIUY/) LIU Y.  
 (CHEN/) CHEN G.  
 XX  
 PI Zhang FL, Luo L, Gustafson E, Liu Y, Chen G;  
 XX  
 DR WPI: 2002-082414/11.  
 DR N-PSDB; ABA92641.  
 XX

XX Identifying modulators of mammalian G-Protein Coupled Receptor SP168,  
 PT useful for treating Parkinson's Disease, Alzheimer's Disease,  
 PT Huntington's Disease, amyotrophic lateral sclerosis and multiple  
 PT sclerosis -  
 XX  
 PS Claim 3; Page 14-15; 16pp; English.

XX The present invention describes a method for identifying agonists and  
 CC antagonists of mammalian G-Protein Coupled Receptor (GPCR) SP168 which  
 CC may be used to treat neurodegenerative disorders. The method comprises:  
 CC (a) contacting a mammalian SP168 receptor (or a functional fragment) in  
 CC the presence of a known amount of a labeled SP168 receptor ligand with  
 CC a sample to be tested for the presence of the SP168 receptor agonist or  
 CC antagonist; and (b) measuring the amount of labeled SP168 ligand  
 CC specifically bound to the receptor (the SP168 receptor agonist or  
 CC antagonist in the sample is identified by measuring the difference in  
 CC binding of the labeled SP168 receptor ligand to the receptor, compared  
 CC to what would be measured in the absence of such agonist or antagonist).  
 CC The method is used to detect agonists and antagonists (especially  
 CC antibodies) of the SP168 GPCR which may be used to treat a  
 CC neurodegenerative disorder, such as Parkinson's Disease, Alzheimer's  
 CC Disease, Huntington's Disease, amyotrophic lateral sclerosis (ALS) and  
 CC multiple sclerosis (MS) in mammals, especially humans. The present  
 CC sequence represents the human SP168 receptor which can be used in the  
 CC method of the invention.  
 XX

Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5,3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 MQAVDNLTSAFGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 DB 1 MQAVDNLTSAFGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 QY 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFVQVTSVIFFTMYISISFLGLITI 120  
 DB 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTRPRPKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRDNKVKCSFLKS 180  
 DB 121 DRYQKTRPRPKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRDNKVKCSFLKS 180  
 QY 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVGKVPKKNVKKVFI 240  
 DB 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVGKVPKKNVKKVFI 240  
 QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342

RESULT 12  
 AAG80236  
 ID AAG80236 standard; Protein; 342 AA.  
 AC AAG80236;  
 DT 24-JAN-2002 (first entry)  
 DE Human PAFR3 protein.  
 KW PAFR-3; platelet activating factor receptor; human; chromosome 3;  
 KW thrombocyte activation; hypotension; renal disease; vascular permeability;  
 KW bronchoconstriction; transgenic animal; knockout animal.  
 OS Homo sapiens.  
 PN DE10020073-A1.  
 XX 25-OCT-2001.  
 XX 22-APR-2000; 2000DE-1020073.  
 XX 22-APR-2000; 2000DE-1020073.  
 PA (BRUE/) BRUESS M.  
 PA (BOEN/) BOENISCH H.  
 FI Bruess M, Boenisch H;  
 DR WPI; 2002-027296/04.  
 DR N-PSDB; RAI68802, RAI68803.  
 XX New human platelet-activating factor (PAF) receptor-3 gene, useful for  
 PT diagnosis and treatment of PAF-related diseases  
 XX  
 PS Disclosure; Page 4; 6pp; German.  
 XX  
 CC This invention describes a novel human platelet-activating factor (PAF)  
 CC receptor-3 (PAFR-3) gene (I). The protein encoded by (I) probably  
 CC modulates the activity of PAF, which is involved in many  
 CC (patho)physiological processes, e.g., thrombocyte activation,  
 CC hypotension, increased vascular permeability, bronchoconstriction etc.  
 CC (I), and derived (anti)sense oligonucleotides, are useful in the  
 CC treatment and diagnosis of (I)-related diseases; for producing  
 CC transgenic/knockout animals, and for recombinant expression of the  
 CC protein (II) that it encodes. (II) is useful in ligand-binding studies  
 CC and screening assays, also for treatment and diagnosis of (II)-related

CC diseases. This sequence represents the human platelet-activating  
 CC factor receptor (PAFR-3) protein described in the invention.  
 XX  
 SQ Sequence 342 AA;  
 Query Match 100.0%; Score 1778; DB 23; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MQAVDNLTSAFGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 DB 1 MQAVDNLTSAFGNTSLCTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFPQIRSKSNFI 60  
 QY 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFVQVTSVIFFTMYISISFLGLITI 120  
 DB 61 IFLKNTVISDLLMLTTPFKILSDAKLGTGRLTFVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTRPRPKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRDNKVKCSFLKS 180  
 DB 121 DRYQKTRPRPKTSNPKNLLGAKILSVVWAFMFLSLPNMILNRPDRDNKVKCSFLKS 180  
 QY 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVGKVPKKNVKKVFI 240  
 DB 181 EFGLVWHEIYVNYICQVIFWFLNFIIVCYTLITKELYSVVRTRGVGKVPKKNVKKVFI 240  
 QY 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 DB 241 IIAVFFICFVFPFHARIPYTLISQTRDVFDCDAENTLFYVKESTLWLTSLNACLDPIYFF 300  
 QY 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342  
 DB 301 LCKSFRNSLISMLKCPNSATSLSDNRKKEQDGDNPNEETPM 342

RESULT 13  
 ABP81734  
 ID ABP81734 standard; Protein; 342 AA.  
 AC ABP81734;  
 DT 04-MAR-2003 (first entry)  
 DE Human P2Y12 platelet ADP receptor protein SEQ ID NO:643.  
 XX  
 KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;  
 KW G protein-coupled receptor modulator; antibody; immune-related disease;  
 KW growth-related disease; cell regeneration-related disease; AIDS; cancer;  
 KW immunological-related cell proliferative disease; autoimmune disease;  
 KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;  
 KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;  
 KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;  
 KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;  
 KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;  
 KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;  
 KW ulcer.  
 OS Homo sapiens.  
 XX  
 PN WO200261087-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 19-DEC-2001; 2001WO-US50107.  
 XX  
 PR 19-DEC-2000; 2000US-257144P.  
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.  
 XX  
 PI Burner GC, Roush CL, Brown JP;  
 XX  
 DR WPI; 2003-046718/04.  
 DR N-PSDB; ABZ42580.  
 XX

PT New isolated antigenic peptides e.g., for G protein-coupled receptors  
 PT (GPCR), useful for diagnosing and designing drugs for treating  
 PT conditions in which GPCRs are involved, e.g. AIDS, Alzheimer's disease,  
 PT cancer or autoimmune diseases

XX Disclosure, Fig 1, 523pp; English.

XX The present invention describes antigenic peptides (I) comprising:  
 CC (a) any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino  
 CC acids. Also described: (1) an assay for the detection of a particular  
 CC G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;  
 CC and (2) an isolated antibody having high specificity and high affinity  
 CC or avidity for a particular GPCR. (1) can be used as GPCR modulators and  
 CC in gene therapy. The antigenic peptides for GPCRs are useful in detecting  
 CC an antibody against a particular GPCR, and in the production of specific  
 CC antibodies. The peptides and antibodies are also useful for detecting the  
 CC presence or absence of corresponding GPCRs. The antigenic peptides for  
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for  
 CC treating immune-related diseases, growth-related diseases, cell  
 CC regeneration-related diseases, immunological-related cell proliferative  
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,  
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,  
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute  
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host  
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,  
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory  
 CC loss, epilepsy, asthma, tuberculosis, obesity, diabetes, hypertension,  
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or  
 CC any other disorder in which GPCRs are involved. The antibodies may be  
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode  
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the  
 CC exemplification of the present invention.

XX Sequence 342 AA;

Query Match 100.0%; Score 1778; DB 24; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-187;  
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRSKSNFI 60  
 DB 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 DB 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTTTRPFKTSNPKNLGKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKS 180  
 DB 121 DRYQKTTTRPFKTSNPKNLGKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKS 180  
 QY 181 EFLGVWHEIVNYICQVIFWNLFIIVICVTLITKELYSYVTRGVGVKPKNVKVF 240  
 DB 181 EFLGVWHEIVNYICQVIFWNLFIIVICVTLITKELYSYVTRGVGVKPKNVKVF 240  
 QY 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVTAENTLFYVKGSTLWLTSLNACLDPFYFF 300  
 DB 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVTAENTLFYVKGSTLWLTSLNACLDPFYFF 300  
 QY 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342  
 DB 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342

RESULT 14.

AA94445

ID AA94445 standard; Protein; 342 AA.

XX AC

XX AA94445;

DT 21-AUG-2000 (first entry)

DE Macaque ortholog of human 15625 receptor protein.

XX Human; G-protein-coupled receptor; GPCR; 15625 receptor protein;  
 KW glial cells; spleen; colon; liver; brain; T-cell; heart;  
 KW red cell; thymus; B-cell; pancreas; disorder; chromosome 3;  
 KW anaemia; neutropenia; thrombocytopenia; gene therapy; ss.

XX Macaca sp.

XX WO200028028-A1.

XX 18-MAY-2000.

XX 05-NOV-1999; 99WO-US25956.

XX 06-NOV-1998; 98US-0187134.

XX 25-AUG-1999; 99US-0382918.

XX (WILL-) MILLENNIUM PHARM INC.

XX Glucksmann MA, Gu W, Weich NS;

XX WPI; 2000-376543/32.

XX N-PSDB; AAA27127.

XX Identifying an agent modulating the level or activity of G-protein  
 PT coupled receptor useful for screening a cell derived from a subject  
 PT having disorders such as anaemia, neutropenia and thrombocytopenia  
 PS Disclosure; Page 90-92; 97pp; English.

XX The 15625 receptor protein is a novel G-coupled protein receptor (GPCR).  
 CC The cDNA for this protein was isolated by screening a human cDNA library  
 CC with sequences homologous to other GPCRs. The 15625 receptor protein is  
 CC expressed in the glial cells of the brain. It is also expressed in  
 CC several other tissues. The 15625 receptor protein may be useful for  
 CC producing antibodies which can be used to detect the presence of the  
 CC receptor protein. The 15625 receptor protein polynucleotides are useful  
 CC for generating probes, primers and antisense constructs. The  
 CC polynucleotides encoding the 15625 receptor proteins can also be inserted  
 CC into vectors to be used in gene therapy. The disorder that may be  
 CC treated using the 15625 receptor protein polynucleotides and  
 CC polypeptides include anaemia, neutropenia and thrombocytopenia. The  
 CC present sequence is the macaque ortholog of the human 15625 receptor  
 CC protein.

XX Sequence 342 AA;

Query Match 98.3%; Score 1748; DB 21; Length 342;  
 Best Local Similarity 98.0%; Pred. No. 1.1e-183;  
 Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRSKSNFI 60  
 DB 1 MQAVNLTSAAGNTSLCTRDYKIQVLPFLYTVLFFVGLITNGLAMRIFQIRSKSNFI 60  
 QY 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 DB 61 IFLKNTVISDLMLITFFPKILSDAKLGTGRLTFCVQVTSVIFFTMYISISFLGLITI 120  
 QY 121 DRYQKTTTRPFKTSNPKNLGKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKS 180  
 DB 121 DRYQKTTTRPFKTSNPKNLGKILSVIWAFFLLSLPNMILTNRQPRDKNVKCSFLKS 180  
 QY 181 EFLGVWHEIVNYICQVIFWNLFIIVICVTLITKELYSYVTRGVGVKPKNVKVF 240  
 DB 181 EFLGVWHEIVNYICQVIFWNLFIIVICVTLITKELYSYVTRGVGVKPKNVKVF 240  
 QY 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVTAENTLFYVKGSTLWLTSLNACLDPFYFF 300  
 DB 241 IIAVFFICFVPHFARIPTLTSQTRDVFDCVTAENTLFYVKGSTLWLTSLNACLDPFYFF 300  
 QY 301 LCKSFNSLSMLKCPNSATSLSQNRKKEQGGDPNEETPM 342

Db 301 LCKSPRNSLSMLKCPNSATSSQDNKRKKQDGPNEETPM 342

RESULT 15

AAE04385

ID AAE04385 standard; Protein; 315 AA.

XX AAE04385;

AC AAE04385;

DT 04-SEP-2001 (first entry)

XX Human P2-purinergic receptor subtype, P2Y12 protein fragment.

DE Human; P2-purinergic receptor; P2Y12; cardiant; vasotropic; thrombolytic;

XX cerebroprotective; synecological; ADP; adenosine 5'-diphosphate; angina;

KW myocardial infarction; ischaemic attack; preelampsia; bleeding disorder;

KW carotid endarterectomy; vascular graft surgery; brain disorder; migraine;

KW vascular injury; schizophrenia; eating disorder; depression; angioplasty;

KW peripheral vascular disease; platelet aggregation; restenotic; embolism;

KW thrombocytopenic purpura; stroke; pertussis toxin-sensitive G protein;

KW Gi; disseminated intravascular coagulation; thrombosis.

XX Homo sapiens.

OS WO200146454-A1.

XX 28-JUN-2001.

XX 26-DEC-2000; 2000WO-US34998.

XX 23-DEC-1999; 99US-0171622.

XX (CORT-) COR THERAPEUTICS INC.

XX Conley PB, Jantzen H, Ramakrishnan-Dubridge V, Julius DJ;

PI Hollopetter G;

XX WPI; 2001-418082/44.

XX N-PSDB; AAD08694.

XX Novel isolated ADP receptor, termed P2Y12 receptor polypeptide, useful

PT for identifying binding partners and for diagnostic applications

XX Example 1; Page 84-85; 108pp; English.

PS The invention relates to ADP (adenosine 5'-diphosphate) receptor, termed

CC as P2Y12 receptor and its corresponding cDNA molecule. P2Y12 receptor is

CC the subtype of P2-purinergic receptor. The P2Y12 receptor is expressed

CC selectively in the platelets and brain, and couples to a pertussis toxin-

CC sensitive G protein (Gi). P2Y12 receptor is a G protein-coupled receptor

CC that responds to ADP. The invention also relates to a method for

CC identifying an agent which is useful for modulating acute myocardial

CC infarction, unstable angina, chronic stable angina, transient ischaemic

CC attacks, strokes, peripheral vascular disease, preelampsia, deep venous

CC thrombosis, embolism, disseminated intravascular coagulation, thrombotic

CC thrombocytopenic purpura or a bleeding disorder; thrombotic and

CC restenotic complications following angioplasty, carotid endarterectomy,

CC post CABG (coronary artery bypass graft) surgery, vascular graft surgery,

CC stent placements or insertion of endovascular devices and prostheses.

CC P2Y12 receptor is useful for identifying binding partners and for

CC diagnostic applications. P2Y12 receptor provides targets for screening

CC synthetic small molecules and combinatorial or naturally occurring

CC compound libraries to regulate platelet aggregation, vascular injury, or

CC disease as well as schizophrenia, eating disorders, depression, migraine

CC and other brain disorders. The present sequence is a fragment of human

CC P2-purinergic receptor subtype, referred as P2Y12.

XX Sequence 315 AA;

SQ

Query Match

Best Local Similarity 91.9%; Score 1634; DB 22; Length 315;

Matches 315; Conservative 100.0%; Pred.No.3.4e-171; Indels 0; Gaps 0;

QY	1	MOAVDNLTAPGNTSLCTRDYKXITQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI	60
Db	1	MOAVDNLTAPGNTSLCTRDYKXITQVLPFLYTVLFFVGLITNGLAMRIFQIRKSNFI	60
QY	61	IFLKNVTISDLLMILTFFPKILSDAKLGTGPIRTFVCOVTSVIFVFTWYISISFLGLITI	120
Db	61	IFLKNVTISDLLMILTFFPKILSDAKLGTGPIRTFVCOVTSVIFVFTWYISISFLGLITI	120
QY	121	DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLLSLPNMLTNRQPRDKNVKCSFLKS	180
Db	121	DRYQKTRTPFKTSNPKNLLGAKILSVIWAFFMLLSLPNMLTNRQPRDKNVKCSFLKS	180
QY	181	EFGLVWHELVNYICQVIFWLNFLIVIVCVTLITKELYSYVTRGVGKVPKKNVKVFI	240
Db	181	EFGLVWHELVNYICQVIFWLNFLIVIVCVTLITKELYSYVTRGVGKVPKKNVKVFI	240
QY	241	IIAVFFICFVPPFPHFARIPTVLSQTRDVFDCVTAENTLFTVKESTLWLTSLNACLDPPFIYFF	300
Db	241	IIAVFFICFVPPFPHFARIPTVLSQTRDVFDCVTAENTLFTVKESTLWLTSLNACLDPPFIYFF	300
QY	301	LCKSPRNSLSMLKC	315
Db	301	LCKSPRNSLSMLKC	315

Search completed: February 4, 2004, 14:29:03

Job time : 44 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:26:47 ; Search time 41 Seconds  
(without alignments)  
2152.536 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SODNRKKEQDGPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: sp\_archea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriapi.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1741	97.9	342	6 Q8HXH1	Q8hxh1 macaca fasc
2	1548.5	87.1	347	11 Q8BZV8	Q8bzx8 mus musculus
3	829	46.6	333	4 Q8BPV8	Q8bpv8 homo sapien
4	829	46.6	352	4 Q8IUT5	Q8iut5 homo sapien
5	823	46.3	333	4 Q8TDU7	Q8tdu7 homo sapien
6	794	44.7	337	11 Q9DBI2	Q9dbi2 mus musculus
7	792	44.5	337	11 Q8C412	Q8c412 mus musculus
8	789	44.4	337	11 Q8CAL2	Q8cal2 mus musculus
9	772	43.4	338	4 Q8IVT7	Q8ivt7 homo sapien
10	699.5	39.3	358	4 Q9BZJ8	Q9bzj8 homo sapien
11	694.5	39.1	358	4 Q9BZ21	Q9bz21 homo sapien
12	687	38.6	358	11 Q8CAI7	Q8cai7 mus musculus
13	685.5	38.6	359	11 Q99WT7	Q99wt7 mus musculus
14	559	31.4	228	6 Q9BE53	Q9be53 macaca fasc
15	553.5	31.1	269	4 Q9BXC2	Q9bxc2 homo sapien
16	487	27.4	319	4 Q8IV06	Q8iv06 homo sapien

17	483.5	27.2	319	11 Q8BY85	Q8by85 mus musculus
18	479.5	27.0	319	11 Q8BG55	Q8bg55 mus musculus
19	478.5	26.9	319	11 Q8CIF3	Q8cif3 mus musculus
20	465.5	26.2	317	11 Q8ETN1	Q8etn1 mus musculus
21	448	25.2	176	4 Q9BT61	Q9bt61 homo sapien
22	412.5	23.2	375	11 Q8BY11	Q8by11 mus musculus
23	388.5	21.9	342	6 Q9TTY5	Q9tty5 bos taurus
24	387.5	21.8	342	6 Q9GK76	Q9gk76 capra hircu
25	368.5	20.7	296	6 Q9ITV6	Q9ity6 canis famil
26	365	20.5	342	6 Q9XSD4	Q9xsd4 sus scrofa
27	364	20.5	341	11 Q8C017	Q8c017 mus musculus
28	356	20.0	374	13 Q57466	Q57466 meleagris g
29	351	19.7	344	11 Q8BMC0	Q8bmc0 mus musculus
30	343	19.3	359	13 Q9PVY7	Q9pvyl anguilla an
31	338	19.0	359	6 Q9N0U1	Q9n0u1 ovis aries
32	336	18.9	309	11 Q8R528	Q8r528 mus musculus
33	327.5	18.4	339	4 Q8NS57	Q8ns57 homo sapien
34	322	18.1	359	11 Q9RPP3	Q9rpp3 cavia porce
35	321	18.1	359	6 Q9GLN9	Q9glng pan troglod
36	318.5	17.9	399	11 Q8R311	Q8r311 mus musculus
37	318	17.9	359	4 Q8TBK4	Q8tbk4 homo sapien
38	316.5	17.8	370	11 Q8BKX1	Q8bkx1 mus musculus
39	316	17.8	365	11 Q8BFP3	Q8bfq3 mus musculus
40	314	17.7	400	6 Q9SM54	Q9sm54 macaca fasc
41	313	17.6	370	11 Q8LGG2	Q8lbg2 mus musculus
42	312.5	17.6	400	11 Q8CGM4	Q8cgm4 cavia porce
43	312	17.5	369	11 Q8BUB7	Q8bub7 mus musculus
44	311.5	17.5	355	6 Q8HZN5	Q8hzn5 macaca mula
45	309	17.4	358	13 Q9PUA0	Q9puao acipenser r

## ALIGNMENTS

### RESULT 1

Q8HXH1 PRELIMINARY; PRT; 342 AA.

AC Q8HXH1  
 DT 01-MAR-2003 (TrEMBLrel 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel 23, Last sequence update)  
 DT 01-MAR-2003 (TrEMBLrel 23, Last annotation update)  
 DE Hypothetical protein.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Medulla oblongata;  
 RA Hashimoto K., Osada N., Hida M., Kusuda J., Sugano S.;  
 RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Medulla oblongata;  
 RX MEDLINE=21458551; PubMed=11574149;  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,  
 RA Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Assignment of 118 novel cDNAs of cynomolgus monkey brain to human  
 chromosomes";  
 RL Gene 275:31-37 (2001).  
 DR EMBL; AB037554; BAC11779.1; -  
 KW Hypothetical protein.  
 SQ SEQUENCE 342 AA; 39479 MW; 0869FDD0144A56FC CRC64;

Query Match 97.9%; Score 1741; DB 6; Length 342;

Best Local Similarity 97.7%; Pred. No. 3.4e-140;

Matches 334; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFPVGLITNGLAMRIFPQIRSKNFI 60

DB 1 MQAVDNLTSAPGNTSLCTRDYKIQVLPFLYTVLFPVGLITNGLAMRIFPQIRSKNFI 60

QY 61 IFKNTVWISDLMLTTPFKKLSDAKLTGTLRTFVQVTSVIFFTMYISIFLGLIT 120  
DB 61 IFKNTVWISDLMLTTPFKKLSDAKLTGTLRTFVQVTSVIFFTMYISIFLGLIT 120  
QY 121 DRYQKTRPFTKSNPKNLLGAKILSVIWAFFMFLSLPNMILNRPDRDNVKKCSFLKS 180  
DB 121 DRYQKTRPFTKSNPKNLLGAKILSVIWAFFMFLSLPNMILNRPDRDNVKKCSFLKS 180  
QY 181 EFGVWHEIYNYIQVFWINFLVIVCYLITKELYSYVTRGVKUPKKNVKKVFI 240  
DB 181 EFGVWHEIYNYIQVFWINFLVIVCYLITKELYSYVTRGVKUPKKNVKKVFI 240  
QY 241 IIAVFFCFVFFHARIPYTLISQTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPIYFF 300  
DB 241 IIAVFFCFVFFHARIPYTLISQTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPIYFF 300  
QY 301 LCKSFNLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342  
DB 301 LCKSFNLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342  
RESULT 2  
Q8BZV8 PRELIMINARY; PRT; 347 AA.  
AC Q8BZV8;  
DT 01-MAR-2003 (TREMBlrel. 23, Created)  
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
DE P2V12 platelet ADP receptor homolog.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Colon;  
RX MEDLINE=22354683; PubMed=12466851;  
RA The FANTOM Consortium;  
RA The RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs."  
RL Nature 420:563-573 (2002).  
DR EMBL; AK033448; BAC28294.1; -  
SQ SEQUENCE 347 AA; 39430 MW; F114688377EB25F1 CRC64;  
Query Match 87.1%; Score 1548.5; DB 11; Length 347;  
Best Local Similarity 88.4%; Pred. No. 7.9e-124;  
Matches 298; Conservative 16; Mismatches 22; Indels 1; Gaps 1;  
QY 6 NLTSAPGNTSLCTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKN 65  
DB 12 NTTFSPGNTSLCTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKN 71  
QY 66 TWISDLMLTTPFKKLSDAKLTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYQK 125  
DB 72 TWISDLMLTTPFKKLSDAKLTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYLK 131  
QY 126 TTRPFTKSNPKNLLGAKILSVIWAFFMFLSLPNMILNRPDRDNVKKCSFLKSEFGLV 185  
DB 132 TTRPFTKSNPKNLLGAKILSVIWAFFMFLSLPNMILNRPDRDNVKKCSFLKSEFGLV 191  
QY 186 WHEIYNYIQVFWINFLVIVCYLITKELYSYVTRGVKUPKKNVKKVFIIVAVF 245  
DB 192 WHEIYNYIQVFWINFLVIVCYLITKELYSYVTRGVKUPKKNVKKVFIIVAVF 251  
QY 246 FICFVFFHARIPYTLISQTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPIYFFLCKSF 305  
DB 252 FICFVFFHARIPYTLISQTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPIYFFLCKSF 311  
QY 306 RNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 342  
DB 312 RNSLSMLKCPNSATSLSDNRKKEQDGDNEETPM 347

RESULT 3  
Q8BZV8 PRELIMINARY; PRT; 333 AA.  
AC Q8BZV8;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Putative G-protein-coupled receptor PKSG77 (G-protein coupled receptor  
GPR86) (G-protein-coupled receptor) (G protein-coupled receptor  
GPR86).  
DE GPR86;  
GN PKSG77 OR GPR86 OR GPR94.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Heart;  
RA Wang Y., Gong L.;  
RT "Molecular cloning of PKSG77, a novel gene encoding a putative G-  
protein-coupled receptor."  
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21172992; PubMed=11273702;  
RA Wittenberger T., Schaller H.C., Hellebrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in  
the discovery of new G-protein coupled receptors."  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21458557; PubMed=11574155;  
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,  
Lewis T., Evans J.F., George S.R., O'Dowd B.F.;  
RT "Discovery and mapping of ten novel G protein-coupled receptor  
genes."  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=11546776;  
RA Communi D., Gonzalez N.S., Dethieux M., Brezillon S., Lainoy V.,  
Farmentier M., Boeynaems J.M.;  
RT "Identification of a Novel Human ADP Receptor Coupled to Gi."  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=27641479-41485 (2001).  
DR EMBL; AF345565; AAK29068.1; -  
DR EMBL; AF293368; AAK01864.1; -  
DR EMBL; AF411113; AAL28484.1; -  
DR EMBL; AF406692; AAL01038.1; -  
DR Genes; HGNC:4537; GPR86.  
DR InterPro; IPR000276; GPCR\_Rhodopsn.  
DR Pfam; PF00001; 7tm.1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsn.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
KW Receptor.  
SQ SEQUENCE 333 AA; 38440 MW; F234ABB50016DF34 CRC64;  
Query Match 46.6%; Score 829; DB 4; Length 333;  
Best Local Similarity 49.1%; Pred. No. 1.1e-62;  
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;  
QY 17 CTRDYKITQVLPFLYTLVFPVGLITNGLAMRFFQIRSKSNFIIFLKNVWISDLMLT 76  
DB 15 CPEDTRIVQLVFPALYTVVFLTGILNTALVFWHPSPSSSTFIYLNKTLVADLIMTL 74  
QY 77 FFPKILSDAKLTGTLRTFVQVTSVIFFTMYISIFLGLITIDRYQKTRPFTKSNPK 136  
DB 75 LFPKILSDSLAPLQVRAVCFPSVIFVETMYVGLVGLIAEDRFLKIRPLRNIFLK 134  
QY 137 NLGAKILSVIWAFFMFLSLPNMILNRPDRDNVKKCSFLKSEFGLVWHEIYNYIQV 196  
DB 135 KPVFAKTVSIFWFFLFFISLPMNLSNKEATPSVKKCASLKGPLGKWHQMVNNICOF 194

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QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFA 256
DB 195 IFWTVFILMVFYVIAKVDYSYRKSVDKDRKNNKLEKGVFVAVFVCFAPHFA 254
QY 257 IPYTLSDTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPPIYFPLCKSPNSLSMLKCP 316
DB 255 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTICMDPLIYFLCKKTEKLPQMG--G 312
QY 317 NSATSLSQDNRRKKEQD 332
DB 313 RKTASSQENHSSQTD 328

RESULT 4
Q81UT5
ID Q81UT5 PRELIMINARY; PRT; 352 AA.
AC Q81UT5;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041116; AAH41116.1; -
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 352 AA; 40586 MW; BCABBE1E405872B CRC64;

Query Match 46.6%; Score 829; DB 4; Length 352;
Best Local Similarity 49.1%; Pred. No. 1.2e-62;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFLKNVTISDLMLIT 76
DB 34 CPRDTRIVQLVFPALYTVVFTLGILLNTLALWVFPHPSSSTFIYILKNTLVADLITLM 93
QY 77 PPFKILSDAKLGTGRLTFVQVTSVIFYFTMYISISFLGLITIDRYOKTRPFKTSNPK 136
DB 94 LPFKILSDSLAPQLRAFVCRFSSVIFYETMYGVILGLIAFDRLFKIRPLRNIFLK 153
QY 137 NLGAKILSVIWMFLLSLPNMILNTRQDRKNNKCKSEFLGVWHEIVNYICQV 196
DB 154 KPVFATVSIIFWFLFISLPNLSNKEATPSVKKCSLKGPLGLKHWQNNICQF 213
QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFA 256
DB 214 IFWTVFILMVFYVIAKVDYSYRKSVDKDRKNNKLEKGVFVAVFVCFAPHFA 273
QY 257 IPYTLSDTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPPIYFPLCKSPNSLSMLKCP 316
DB 274 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTICMDPLIYFLCKKTEKLPQMG--G 331
QY 317 NSATSLSQDNRRKKEQD 332
DB 332 RKTASSQENHSSQTD 347

RESULT 5
Q8TDU7
ID Q8TDU7 PRELIMINARY; PRT; 333 AA.
AC Q8TDU7;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Putative G-protein coupled receptor.
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GN GPCR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Takada S., Kadowaki S., Haga T., Takaseu H., Mitaku S.;
RT Identification of G protein-coupled receptor genes from the human
RT genome sequence.
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB083597; BAB9310.1; -
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 333 AA; 38409 MW; 3F88E7EAC9F5428F CRC64;

Query Match 46.3%; Score 823; DB 4; Length 333;
Best Local Similarity 48.7%; Pred. No. 3.6e-62;
Matches 154; Conservative 57; Mismatches 103; Indels 2; Gaps 1;

QY 17 CTRDYKIQVLPFLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFLKNVTISDLMLIT 76
DB 15 CPRDTRIVQLVFPALYTVVFTLGILLNTLALWVFPHPSSSTFIYILKNTLVADLITLM 74
QY 77 PPFKILSDAKLGTGRLTFVQVTSVIFYFTMYISISFLGLITIDRYOKTRPFKTSNPK 136
DB 75 LPFKILSDSLAPQLRAFVCRFSSVIFYETMYGVILGLIAFDRLFKIRPLRNIFLK 134
QY 137 NLGAKILSVIWMFLLSLPNMILNTRQDRKNNKCKSEFLGVWHEIVNYICQV 196
DB 135 KPVFATVSIIFWFLFISLPNLSNKEATPSVKKCSLKGPLGLKHWQNNICQF 194
QY 197 IFWINFLIVVYTLITKELYRSYVTRGVGKVRKKNVKKVFIILIAVFFICVPPHFA 256
DB 195 IFWTVFILMVFYVIAKVDYSYRKSVDKDRKNNKLEKGVFVAVFVCFAPHFA 254
QY 257 IPYTLSDTRDVFDCVTAENTLFFVKESTLWLTSLNACLDPPIYFPLCKSPNSLSMLKCP 316
DB 255 VPYTHSQNNKTDCLQNLQFIKATETTLFLAANTICMDPLIYFLCKKTEKLPQMG--G 312
QY 317 NSATSLSQDNRRKKEQD 332
DB 313 RKTASSQENHSSQTD 328

RESULT 6
Q9DB12
ID Q9DB12 PRELIMINARY; PRT; 337 AA.
AC Q9DB12;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE 2010001106Rik protein.
GN GPR86 OR 2010001106RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yananaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Giesi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
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RA Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barah G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Guscinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL; AK008013; BAB25409.1; -  
DR MGD; MGI:1921441; Gpr86.  
DR InterPro; IPR000276; GPCR\_Rhodopsin.  
DR InterPro; IPR005466; UDG\_receptor.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCR\_Rhodopsin.  
DR PRINTS; PR01655; UDG\_LUCOSER.  
DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
SQ SEQUENCE 337 AA; 38693 MW; 2C1A76FB893D5EA CRC64;

Query Match 44.7%; Score 794; DB 11; Length 337;  
Best Local Similarity 45.9%; Pred. No. 1.1e-59;  
Matches 151; Conservative 63; Mismatches 111; Indels 4; Gaps 3;

QY 6 NLTSAPG--NTSLCTRDYKIQVLFPPLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFL 63  
Db 6 NTTGMOGFKNSERCPRDTRMTQLLPVLYTVVFLAGILLNTVALWVFPSPNSTFIIVL 65

QY 64 KNTVISDLMLITPFPKILSDAKLGTGRLPFCQVTSVIFFTMYISIFLGLITIDRY 123  
Db 66 KNTLVADLIMALMFPKILSDSLAPWQLRGFCVCTLSVVFYETMYGIMMGLIAFDRF 125

QY 124 OKTTRPFTSNPKNLLGAKILSVIWFAMFLLSPNMLITNRQPRDKNVKCKSLKSEFG 183  
Db 126 LKIIMPFRTFKTAPAKTIVSIWSLMFFISLPNML-NKEATPSSVKKCSLKSPLG 184

QY 184 LVWHEIVNYICQVIFWIFNFIIVCYTLITKELYSYVRGVGVKVRKKNVVFIIIA 243  
Db 185 LWWHQVSHSTCOLIFWAVFIIMLLFYAVITKKVNSYRKFRKSDS-RHKLELVKVFVIMA 243

QY 244 VFFICFVFPFHARIPYTLISQTRDVFDCVAENTLFVVKESTLWTLNACLDPFIYFLCK 303  
Db 244 VFFVCFAPLHFRIPYTSQTNKTDCELENQLFAKEATLFLATTNICMDPLIYIILCK 303

QY 304 SFRNLSIMLKCPNSATLSQDNKKKQED 332  
Db 304 KFTQKPCVRWGKARTAGSSEHSSQTD 332

RESULT 7  
Q8C412 PRELIMINARY; PRT; 337 AA.

ID Q8C412  
AC Q8C412;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE G protein-coupled receptor 68 homolog.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
RX MEDLINE=22354683; Pubmed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).  
DR EMBL; AK038560; BAC30043.1;  
SQ SEQUENCE 337 AA; 38755 MW; 70E9AA7B9B089BOA CRC64;

Query Match 44.4%; Score 789; DB 11; Length 337;  
Best Local Similarity 45.6%; Pred. No. 2.9e-59;  
Matches 150; Conservative 63; Mismatches 112; Indels 4; Gaps 3;

QY 6 NLTSAPG--NTSLCTRDYKIQVLFPPLLYTVLFFVGLITNGLAMRIFFOIRSKSNFIIFL 63  
Db 6 NTTGMOGFKNSERCPRDTRMTQLLPVLYTVVFLAGILLNTVALWVFPSPNSTFIIVL 65

QY 64 KNTVISDLMLITPFPKILSDAKLGTGRLPFCQVTSVIFFTMYISIFLGLITIDRY 123  
Db 66 KNTLVADLIMALMFPKILSDSLAPWQLRGFCVCTLSVVFYETMYGIMMGLIAFDRF 125

QY 124 OKTTRPFTSNPKNLLGAKILSVIWFAMFLLSPNMLITNRQPRDKNVKCKSLKSEFG 183  
Db 126 LKIIMPFRTFKTAPAKTIVSIWSLMFFISLPNML-NKEATPSSVKKCSLKSPLG 184

QY 184 LVWHEIVNYICQVIFWIFNFIIVCYTLITKELYSYVRGVGVKVRKKNVVFIIIA 243  
Db 185 LWWHQVSHSTCOLIFWAVFIIMLLFYAVITKKVNSYRKFRKSDS-RHKLELVKVFVIMA 243

QY 244 VFFICFVFPFHARIPYTLISQTRDVFDCVAENTLFVVKESTLWTLNACLDPFIYFLCK 303  
Db 244 VFFVCFAPLHFRIPYTSQTNKTDCELENQLFAKEATLFLATTNICMDPLIYIILCK 303

QY 304 SFRNLSIMLKCPNSATLSQDNKKKQED 332  
Db 304 KFTQKPCVRWGKARTAGSSEHSSQTD 332

RESULT 8  
Q8C412 PRELIMINARY; PRT; 337 AA.

ID Q8C412  
AC Q8C412;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE G protein-coupled receptor 68 homolog.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=Hypothalamus;  
RX MEDLINE=22354683; Pubmed=12466851;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
RL Nature 420:563-573(2002).  
DR EMBL; AK038560; BAC30043.1;  
SQ SEQUENCE 337 AA; 38755 MW; 70E9AA7B9B089BOA CRC64;

Db 185 LWHEQVSHSTQCFIFWAVFIMLMLFYAVITKTVNSYKFRSKDS-RHKLEVRVFVMA 243  
QY 244 VFICFVPFHARIPYTLSTQTRDVPDCTAENTLFYVKESTLWLTSLNACLDPIYFFLCK 303  
Db 244 VFFVCFAPLHVRIPYTSQTNTKDRLENQLFIAKEATFLATINQMDPLIYILCK 303  
QY 304 SFRNSLSMLKCPNSATSLSDNRKXQD 332  
Db 304 KFTQKQPCVRGKARTAGSSSEHSSQTD 332

RESULT 9

Q8IYT7 PRELIMINARY; PRT; 338 AA.  
AC Q8IYT7;  
DT 01-MAR-2003 (TremBLrel. 23, Created)  
DT 01-MAR-2003 (TremBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE G protein-coupled receptor 105.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Testis;  
RA Strausberg R.;  
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC034989; AAH34989.1; -  
KW Receptor.  
SQ SEQUENCE 338 AA; 38972 MW; 8671408E2F392DEB CRC64;

Query Match 43.4%; Score 772; DB 4; Length 338;

Best Local Similarity 47.5%; Pred. No. 8e-58;

Matches 149; Conservative 60; Mismatches 105; Indels 0; Gaps 0;

QY 6 NLTSAPGNTSLCTRDYKITQVLPFLYLVLPFVGLITNGLAMRFFOIRKSNFIPLKN 65  
Db 3 NSTSTQPPDESCQNLIITQIIPVLCWVFIAGILLNGVSGWIFFVPSSEFIYLVKN 62  
QY 66 TVISDLMLITFPFKILSDAKLGTGPTRTVCQVTSVIFFTMYISIFLGLTIDRYQK 125  
Db 63 IVIADFVMSLTFPPEKILGDSGLGQWLNQVFCRVSAVLFYNNVYSIVFFGLISDFRYK 122  
QY 126 TTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMLITNQPDKNVKCSFLKSEPLV 185  
Db 123 IVKPLWTSFIOVSYSKLLSVIWMMLLAVPNIITNQSREVTQIKIELKSELGRK 182  
QY 186 WHEIVNYICQVIFWIFNLIVICVTLITKELYRSYVTRGVKVPKKNVVFIIIAVF 245  
Db 183 WHKASNYIFVAIFWIFVLLIVFTAITKTFKSHLKSRRNSTSVKKSRRNIFSIIVFV 242  
QY 246 FICFVPFHARIPYTLSTQTRDVPDCTAENTLFYVKESTLWLTSLNACLDPIYFFLCKSF 305  
Db 243 FVCFVPHARIPYTSQTEAHYSQSKELRYWKFTLLLSAANVCLDPIYFFLCQPF 302

RESULT 10

Q96JZ8 PRELIMINARY; PRT; 358 AA.  
AC Q96JZ8;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Hypothetical protein FLU14878.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RA Itoai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,  
RA Ninomiya K., Iwayanagi T.,  
RT "NEDO human cDNA sequencing project";  
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
DR EMBL; AK027784; BAB55366.1; -  
DR Genew; HGNC:4538; GPR87.  
DR InterPro; IPR000276; GPCR\_Rhodpsn.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PRO0237; GPCRHHODOPSN.  
DR PROSITE; PS00337; G-PROTEIN RECEPTOR FL1; 1.  
DR PROSITE; PS0262; G-PROTEIN RECEPTOR FL2; 1.  
KW Hypothetical protein; G-protein coupled receptor; Receptor;  
KW Transmembrane.  
SQ SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match 39.3%; Score 699.5; DB 4; Length 358;

Best Local Similarity 42.6%; Pred. No. 1.2e-51;

Matches 140; Conservative 67; Mismatches 113; Indels 9; Gaps 5;

QY 6 NLTSAPG-NTSLCTRDYKITQVLPFLYLVLPFVGLITNGLAMRFFOIRKSNFIPLK 64  
Db 25 NRSDCPGKNTL--HNEFDIVLPVLIIFVASILLNGLAVNFIHNRKTSFIFLK 81  
QY 65 NTVISDLMLITFPFKILSDAKLGTGPTRTVCQVTSVIFFTMYISIFLGLTIDRYQ 124  
Db 82 NTIWAADLMLITFPFRIYVHDAGFGPWFKILCRYTSVLFYANNYTSIVFGLISIDRYL 141  
QY 125 KTRPFTSNPNKLLGAKILSVIWAFFLLSLPNMLITNQPDKNVKCSFLKSEPL 184  
Db 142 KVKPFGSRMYNITFTKVLSCVWVNAVLSLNPILITNGQPTEDNHDCKSLKSLGV 201  
QY 185 WHEIVNYICQVIFWIFNLIVICVTLITKELYRSYVTRGVKVPK-KVNVKVFIIIA 243  
Db 202 KWHATAVTVNSCLFVAVLVILGCVIALSYIHKS--SRQFISQSSRRKKNQSIIRVVA 259  
QY 244 VFICFVPFHARIPYTLSTQTRDVPDCTAENTLFYVKESTLWLTSLNACLDPIYFFLCK 303  
Db 260 VFTTCTPLPHLCRIPFTFTHLDRLDDESAQKILYCKEITLFSACNVCLDPIYFFMCR 319  
QY 304 SFRNSLI--SMLKCPNSATSLSDNRKXE 330  
Db 320 SFSRRLFKKSNIRTSSESIRSLQSVRSE 348

RESULT 11

Q9BY21 PRELIMINARY; PRT; 358 AA.  
AC Q9BY21;  
DT 01-JUN-2001 (TremBLrel. 17, Created)  
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)  
DT 01-MAR-2003 (TremBLrel. 23, Last annotation update)  
DE Orphan G protein-coupled receptor 87.  
GN GPR87 OR GPR95.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21172992; PubMed=11273702;  
RA Wittenberger T., Schaller H.C., Hellebrand S.;  
RT "An expressed sequence tag (est) data mining strategy succeeding in





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Db 86 VADLIMLTTPFRIVRDAGFGPWYFEBILCRYTSVLFYANNYTSIVPLGLISVDRLKVV 145
Qy 128 RPFKTSNPKLLGAKILSVIWAFLSLPMLILNRPDRQXVKCKSLKSEFGLVWH 187
Db 146 KPGDSSWISITFKVLVSVCWVIMAILSPNLIINGQPTKENIHDCMKLSPLGAKWH 205
Qy 188 EIVNYICQVIFWFLNFIIVCYTLITKELYSYVTRGVGKVPK-KVNVKVFIIIAVFF 246
Db 206 MAVTVDSCLFVAVLVILGCIYASRYIHK-SRQFISQSRKKNQSIKRVVAVFF 263
Qy 247 ICFVFFHAFIPIVTLSTQTRVDFCTAENTLIFYKESTLMTLSNACLDPFIIFFLCKSFR 306
Db 264 TCLEPLVHLCPITPFFSNLDRLDESAAKILYYCKEMTLFLSACNVCLDPIIYFFMCKSFS 323
Qy 307 NSLI-SMLKCPNSATSLSDNRKKE 330
Db 324 RRLFKSNIRTSIESIRLSQVRSE 349

RESULT 14
Q9BE53 PRELIMINARY; PRT; 228 AA.
AC Q9BE53
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE "Isolation of full-length cDNA clones from macaque brain CDNA libraries."
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain CDNA libraries."
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056816; BAB39342.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_Fl_2; 1.
SQ SEQUENCE 228 AA; 26356 MW; 47907FSDDEEDD22C CRC64;

Query Match 31.4%; Score 559; DB 6; Length 228;
Best Local Similarity 46.7%; Pred. No. 7.1e-40;
Matches 105; Conservative 40; Mismatches 78; Indels 2; Gaps 1;

Qy 108 MYISISFLGIIIDRYOKTTTPKTSNPKLLGAKILSVIWAFLSLPMLILNRPQ 167
Db 1 MYGIVLGLIAFRFLKIRLIRNIFLKTQVFAKTSVPIWISFFFLSLPMLILNKEA 60
Qy 168 RDNKVKCKSLKSEFGLVWHIEIVNYICQVIFWFLNFIIVCYTLITKELYSYVTRGVG 227
Db 61 TESSVKKCASLKGPLGKHLQVNNISQPIFWFVLMVYVVIKQVYDSYKSKSD 120
Qy 228 KVPKKNVNVKVFIIIAVFFICFPFHAFIPIVTLSTQTRVDFCTAENTLIFYKESTLMT 287
Db 121 RKNKCKLGKGVVAVVAVFFVCFAPFHFTFVPTVYTSQTNKDKRLQNLFIKETTFLA 180
Qy 288 SLNACLDPFIYFFLCKSFRNLSLMLKCPNSATSLSDNRKKEQD 332
Db 181 ATNLCMDPLIYIFLCKKFTKLPQMRGRKTIAS--SQENSSQTD 223

RESULT 15
Q9BXC2 PRELIMINARY; PRT; 269 AA.
ID Q9BXC2
AC Q9BXC2;
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Putative G-protein-coupled receptor FKSG78 (G protein-coupled receptor 87).
GN FKSG78.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Wang Y.-G, Gong L.;
RT "Identification of FKSG78, a novel gene encoding a putative G-protein-coupled receptor."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AP345566; AA029069.1; -
DR EMBL; BC009540; AA009540.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm 1; 1.
DR PRINTS; PR00237; GPCR_Rhodpsn.
DR PROSITE; PS00237; G PROTEIN RECP Fl 1; 1.
DR PROSITE; PS0262; G-PROTEIN_RECP_Fl_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 269 AA; 31443 MW; 1E7D498EE20717F6 CRC64;

Query Match 31.1%; Score 553.5; DB 4; Length 269;
Best Local Similarity 42.5%; Pred. No. 2.4e-39;
Matches 111; Conservative 50; Mismatches 95; Indels 5; Gaps 3;

Qy 73 MLITFPFKILSDAKLGHCPLETFVQCQTSVIFFTWYISIFLGLITIDRYOKTRPPT 132
Db 1 MTLTFPFRIVHDAGFGPWYFEBILCRYTSVLFYANNYTSIVPLGLISVDRLKVV 60
Qy 133 SNPKLLGAKILSVIWAFLSLPMLILNRPDRQXVKCKSLKSEFGLVWHIEIVNY 192
Db 61 SRMYSITFTKVLSCVWVIMAILSPNLIINGQPTKENIHDCMKLSPLGAKWHAVTY 120
Qy 193 ICQVIFWFLNFIIVCYTLITKELYSYVTRGVGKVPK-KVNVKVFIIIAVFFICFP 251
Db 121 VNSCLFVAVLVILGCIYASRYIHK-SRQFISQSRKKNQSIKRVVAVVFFTCFLP 178
Qy 252 FHPARIPTLSQTRVDFCTAENTLIFYKESTLMTLSNACLDPFIIFFLCKSFRNLSI- 310
Db 179 YHLCRIPTFSLDLRLDESAAKILYYCKEMTLFLSACNVCLDPIIYFFMCKSFRLEK 238
Qy 311 -SMLKCPNSATSLSDNRKKE 330
Db 239 KSNIRTSIESIRLSQVRSE 359

Search completed: February 4, 2004, 14:30:26
Job time : 42 secs
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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:27:22 ; Search time 20 Seconds

(without alignments)

1644.484 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNKKKQDGGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 76:.\*  
1: Piri:.\*  
2: Piri2:.\*  
3: Piri3:.\*  
4: Piri4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	394	22.2	342	2 A40191	platelet-activatin
2	392.5	22.1	342	2 S13638	platelet-activatin
3	379.5	21.3	361	2 B45580	G protein-coupled
4	366	20.6	341	2 S63866	platelet activatin
5	362	20.4	341	2 S43252	platelet-activatin
6	357.5	20.1	308	2 I50241	G protein-coupled
7	339	19.1	359	2 S15403	angiotensin II rec
8	338	19.0	344	2 T09508	intrin 17 purinerg
9	329	18.5	359	2 I39418	angiotensin II rec
10	325	18.3	359	2 S44425	angiotensin II rec
11	325.5	18.3	399	2 I48705	proteinase activat
12	325	18.3	359	2 A48857	angiotensin II rec
13	321	18.1	359	2 J11104	angiotensin II rec
14	321	18.1	370	2 JC5549	heptahelical P2ys
15	319	17.9	359	2 A42656	angiotensin II rec
16	319	17.9	359	2 JC2134	angiotensin II rec
17	318	17.9	359	2 JH1194	angiotensin II rec
18	318	17.9	359	2 JH0821	angiotensin II rec
19	317.5	17.9	365	2 S68208	G protein-coupled
20	317.5	17.9	398	2 I56517	mu opiod receptor
21	314.5	17.7	398	2 I56504	mu opiod receptor
22	314	17.7	359	2 JQ1516	angiotensin II rec
23	313.5	17.6	380	2 I38435	angiotensin recept
24	310.5	17.5	362	2 JN0694	angiotensin II rec
25	309	17.4	392	2 S65893	opiod receptor mu
26	309	17.4	400	2 I56553	mu opiate receptor
27	306	17.2	397	2 S66518	proteinase-activat
28	304.5	17.1	398	2 A57510	mu opiod receptor
29	299	16.8	380	2 JC2434	kappa opiod recep

G protein-coupled  
kappa opiod recep  
angiotensin II rec  
interleukin-8 rece  
kappa opiod recep  
thrombin receptor  
kappa opiod recep  
kappa opiod recep  
ATP receptor P2u -  
neuropeptide Y/pep  
G protein-coupled  
fusin (LESTRA) - c  
chemokine (C-C) re  
interleukin-8 rece  
neuropeptide Y/pep

## ALIGNMENTS

### RESULT 1

A40191  
platelet-activating factor receptor - human  
C:Species: Homo sapiens (man)  
C>Date: 28-Aug-1992 #sequence revision 28-Aug-1992 #text change 20-Jun-2000  
C/Accession: A40191; JH0479; A41079; JCI359; A42831; I51923  
R/Kunz, D.; Gerard, N.P.; Gerard, C.  
J. Biol. Chem. 267, 9101-9106, 1992  
A/Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell su  
A/Reference number: A40191; MUID:92250505; PMID:1374385  
A/Accession: A40191  
A/Molecule type: mRNA  
A/Residues: 1-342 <KUN>  
A/Cross-references: GB:M76674; NID:G456293; PIDN:AAA60002.1; PID:G456294  
R.Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochran, C.G.  
Biochem. Biophys. Res. Commun. 180, 105-111, 1991  
A/Title: Characterization of a human cDNA that encodes a functional receptor for platelet  
A/Reference number: JH0479; MUID:92028922; PMID:1656963  
A/Accession: JH0479  
A/Molecule type: mRNA  
A/Residues: 1-342 <YER>  
A/Cross-references: GB:M80436; NID:G189537; PIDN:AAA60001.1; PID:G189538  
R.Nakamura, M.; Honda, Z.; Izumi, T.; Sakanaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Se  
J. Biol. Chem. 266, 20400-20405, 1991  
A/Title: Molecular cloning and expression of platelet-activating factor receptor from hu  
A/Reference number: A41079; MUID:92041873; PMID:1657923  
A/Accession: A41079  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 1-342 <NAK>  
A/Cross-references: GB:D10202; GB:D90433; NID:G219975; PIDN:BAA01050.1; PID:G219976  
R.Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.  
Biochem. Biophys. Res. Commun. 189, 617-624, 1992  
A/Title: Molecular cloning and characterization of the platelet-activating factor recep  
A/Reference number: JCI359; MUID:93112021; PMID:1281995  
A/Accession: JCI359  
A/Molecule type: mRNA  
A/Residues: 1-315, 'N', 317-342 <SUG>  
A/Experimental source: heart  
A/Note: the authors translated the codon AAT for residue 316 as Lys  
Riseyfried, C.B.; Schweickart, V.L.; Godiska, R.; Gray, P.W.  
Genomics 13, 832-834, 1992  
A/Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns  
A/Reference number: A42831; MUID:92347886; PMID:1322356  
A/Accession: A42831  
A/Molecule type: DNA  
A/Residues: 1-226, 'TG', 229-342 <SEV>  
A/Cross-references: GB:M88177; NID:G190697; PIDN:AAA60214.1; PID:G190698  
A/Note: sequence extracted from NCI backbone (NCBIN:109813, NCBIF:109814)  
R.Chase, P.B.; Halonen, M.; Regan, J.W.  
Am. J. Respir. Cell Mol. Biol. 8, 240-244, 1993

A>Title: Cloning of a human platelet-activating factor receptor gene: evidence for an intracellular domain  
A/Reference number: I51923; MUID:93192035; PMID:8383507

A/Accession: I51923

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-342 <RES>

A/Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581

C/Genetics:

A/Gene: GDB:PTAFR

A/Cross-references: GDB:128806; OMIM:173393

A/Map position: lp35-lp34.3

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; transmembrane protein

P:17-38/Domain: transmembrane #status predicted <TRI>

P:54-75/Domain: transmembrane #status predicted <VII>

P:92-113/Domain: transmembrane #status predicted <III>

P:134-155/Domain: transmembrane #status predicted <TRV>

P:184-205/Domain: transmembrane #status predicted <TRV>

P:233-253/Domain: transmembrane #status predicted <TVI>

P:277-297/Domain: transmembrane #status predicted <VII>

Query Match 22.2%; Score 394; DB 2; Length 342;

Best Local Similarity 32.6%; Pred. No. 1.5e-26;

Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;

QY 11 PGNTSLCTRDYKITQVLPFLLYTLVFFVGLITNGLAMRIFFQIR--SKSNFI-IFLKNTV 67

DB 3 PHDSHMDSEPRYT--LFFIVYSIFVGLVANGYLVWVFLVYVPCCKFEIKIFWVNL 60

QY 68 ISDLMLITPFPKLSDAKLTGTLRTVFCQVTSVIFYFMYISISLGLITIDRYOKIT 127

DB 61 MADLFLITPLWIVYQNGNWILPKFLCNVACGLFFINTYCSVAFGLVITNRFQAV 120

QY 128 RPFKTSNPKNLGAKILSVIWI-----AFMFLSLPNNMILTNQPRDK---NVYKGSFLK 179

DB 121 RPIKTAQANTKRGISLSLVWVAVGAASVFLIDS---TNTVDSAGSGNVTTC-FEH 176

QY 180 SEGLVWHEIVNYCCQVIFWNLIVIVCYTLITKELYRVSRTGVRGKVPKKNVQVP 239

DB 177 YKGSVPVLIITHIFVFSFVFLVILFCNLVILVITLQMPVQOQNAEYKRALWV-VC 235

QY 240 IIAVFFICFPVFPFARIPYTLSTQTRVDCTAENTLFFYKESLWLTSLNACLDPEIYF 299

DB 236 TVLAVFICFPVHVQVLPWLAEI-LGQDSKFPQAHQVTLCLSTNCVLDPIYIC 294

QY 300 FLCKSRN-----SLISMLKCPNSAT 320

DB 295 FLTKFKRHLTEKFYSMRSSKCRATT 322

RESULT 2

S13638

C/Species: Cavia porcellus (guinea pig)

C/Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 08-Oct-1999

C/Accession: S13638

R/Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.; To

Nature 349, 342-345, 1991

A>Title: Cloning by functional expression of platelet-activating factor receptor from gu

A/Reference number: S13638; MUID:91101726; PMID:1846231

A/Accession: S13638

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-342 <CON>

A/Cross-references: GB:X56736; NID:g49442; PIDN:CAA40060.1; PID:g49443

A/Note: the species of guinea pig is not identified; in GenBank entry CCPAFREC, release

C/Superfamily: ATP receptor P2u

Query Match 22.1%; Score 392.5; DB 2; Length 342;

Best Local Similarity 30.7%; Pred. No. 2.1e-26;

Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY 20 DYKITQVLPFLLYTLVFFVGLITNGLAMRIFFQI--RSKSNFI-IFLKNTVISDLMLIT 76

DB 10 DSEPRYLPFIVISIIIFVGLIANGYVWVFAKLYPSKLNKIKIFWNLTVADLLFLIT 69

QY 77 FPFKILSDAKLTGTLRTVFCQVTSVIFYFMYISISLGLITIDRYOKTRPFTSNPK 136

DB 70 LPLMIVYSNQGWNFLPKFLCNLACGLFFINTYCSVAFGLVITVNRFPQAVKYPKTAQAT 129

QY 137 NLLGAKILSVIWI-----AFMFLSLPNNMILTNQPRDKKVKKCSLKSSEFG---LVWH 187

DB 130 TRKGIALSLVIVAVIAAASVFLVMDSTNVSNKAGSGNITRC-FEYKSGKPVLIH 188

QY 188 EIVNYICQVI-FWINFLIVIVCYTLITKELYRVSRTGVRGKVPKKNVVKVFIIVAVFF 246

DB 189 -----ICVLGFFVFLVILFCNLVILITLRLQPVKQORNAEV-RRRALWVCTVLAVFV 242

QY 247 ICYVFPFARIPYTLSTQTRVDCTAENTLFFYKESLWLTSLNACLDPEIYFELCKSER 306

DB 243 ICYVPHHVQVLPWLAEI-LGQDSKFPQAHQVTLCLSTNCVLDPIYICFLTCKKR 301

QY 307 NSLISMLKCPNSATSLSQDNRRKKEQDGDGDPNEETPM 342

DB 302 KHLSEKLNIMSGSKSRVTTDTGTETMAIPINHPTFV 337

RESULT 3

B45680

G protein-coupled peptide receptor EBI 2 - human

C/Species: Homo sapiens (man)

C/Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000

C/Accession: B45680

R/Birkenbach, M.; Josefsen, K.; Yamamachi, R.; Lenoir, G.; Kieff, E.

J. Virol. 67, 2209-2220, 1993

A/Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-coupled

A/Reference number: A45680; MUID:93188173; PMID:8383238

A/Accession: B45680

A/Status: preliminary

A/Molecule type: nucleic acid

A/Residues: 1-361 <BIR>

A/Cross-references: GB:L08177; NID:g292056; PIDN:AAA35924.1; PID:g292057

A/Experimental source: B-lymphocytes

A/Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBI:127097)

C/Superfamily: ATP receptor P2u

C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match 21.3%; Score 379.5; DB 2; Length 361;

Best Local Similarity 26.0%; Pred. No. 2.9e-25;

Matches 94; Conservative 84; Mismatches 152; Indels 31; Gaps 11;

QY 1 MQAVDNLT---SAPGNTSLCTRDYKITQVLPFLLYTLVFFVGLITNGLAMRIFFQIRSK 56

DB 3 IQMANNFTPPSATPGNDCDLVAHSTARIWPLHYSILVFIIGLVGNLLALVAVIQNRKK 62

QY 57 SN-FIIFLKNVTISDLMLITFPFKIL-----SDAKLTGTLRTVFCQVTSVIFYFMYI 110

DB 63 INSTLYSLNVLISDLITFTLPTALPTRIAYANGFDWRIGDA-----LCRTALVFIINTYA 117

QY 111 SISPLGLITIDRYOKTRPFTSNPKNLGAKILSVIWIWAFMFLSLPNNI--LTNRQPR 168

DB 118 GVNFTCLSIDRFIAVHPLAVNKKIRIEHAKGVCIFWILVFAQTLLPLINPMKQEA 177

QY 169 DKNVKKCSLKSBEGLVWHEIVNYCQVIFWNLIVIVCYTLITKELYRS-----YVRT 223

DB 178 RITCMEYFPNFEETKSLPW--ILLGACFGYVLPVILILICYSQICCKLFRPAKQNPITEK 235

QY 224 RGVGKVPKKNVKNVFIIVAVFFICFPVFPFARIPYTLSTQTR--DVFDCTAENTLFFYK 281

DB 236 SCVKN--KALNT-IILIIIVFVLCFTFVHVAIIQHEMKLKRFSNFECSQRHFSQISLH 291

QY 282 STLWLTSLNACLDPEIYFELCKSRFNSLSMLKCPNSATSLSQDNRRKKEQDGDGDPNEETP 341

DB 292 FTVCLMNFNCMDPPIYFACKYKRWMLK-RQVSVSISAVKGAPEENSREMTETQ 350

QY 342 M 342

Db 351 M 351

## RESULT 4

S63666  
platelet activating factor receptor - mouse

C:Species: Mus musculus (house mouse)

C&gt;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000

C:Accession: S63666

R:Ishii, S.; Matsuda, Y.; Nakamura, M.; Waga, I.; Kume, K.; Izumi, T.; Shimizu, T.

Biochem. J. 314, 671-678, 1996

A:Title: A murine platelet-activating factor receptor gene: cloning, chromosomal localization

A:Reference number: S63666; MUID:96233129; PMID:8670084

A:Accession: S63666

A&gt;Status: preliminary

A:Molecule type: DNA

A:Residues: 1-341 &lt;ISH&gt;

A:Cross-references: EMBL:D50872; NID:g1256924; PIDN:BAA09468.1; PID:g1256925

C:Superfamily: ATP receptor P2u

Query Match 20.6%; Score 366; DB 2; Length 341;

Best Local Similarity 29.9%; Pred. No. 4e-24;

Matches 96; Conservative 64; Mismatches 133; Indels 28; Gaps 10;

Qy 20 DYKITQVLFPLLYTVLFFVGLITNGLAMRIFFOI--RSKSNFI-IFLKNVTVIDLLMILT 76

Db 10 DSEFRYTLFPIVYGVIFILGVVANGYVILWVFNLYPSKLNKIKIFWNLTMADLLFLIT 69

Qy 77 PPKILSDAKLGTGPTLFTVCQVTSVIFYFTMYISIFLGLITIDRYOKTRPFTSNPK 136

Db 70 LPLMIVYYNEGDWILFNLCNAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQAT 129

Qy 137 NLLGAKILSVVWAFM-----FILSLPNMILTNRQPRDKNVKCSFLKSEFG--LWVHE 188

Db 130 TRKGISLSLIWISIVATASYFLATSTNVLPKOGSGNITRCFEHYEPYSVILVHV 189

Qy 189 INVNICQVIFWNLFI-VIVCYTLITKELYSYVTRGVGVKPRKKNVVFIIIVFFI 247

Db 190 FIACFFLVFFLIYFCNLVLIHTLTQPMRQQ--RKAGV----KRALMWVCTVLAFFII 243

Qy 248 CFVPEFHPIRYITLSQTRDVFDCATENTLFVVKESTLWLTSLNACLDPEIYFFLCKSF 307

Db 244 CFVPHVVLFWTLIAELG--YQTFHQAINDAHQITLCLSTNCVLDPIYCFLTCKFRK 301

Qy 308 -----SLISMLKCPNSATS 321

Db 302 HLSEKFKYSMRSRKC-SRATS 321

RESULT 5

S43252

platelet-activating factor receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C&gt;Date: 20-Oct-1994 #sequence\_revision 10-Nov-1995 #text\_change 24-Nov-1999

C:Accession: S43252

R:BiCo, H.; Honda, Z.; Nakamura, W.; Shimizu, T.

Eur. J. Biochem. 221, 211-218, 1994

A:Title: Cloning, expression and tissue distribution of rat platelet-activating-factor-

A:Reference number: S43252; MUID:94222063; PMID:8168510

A:Accession: S43252

A:Molecule type: mRNA

A:Residues: 1-341 &lt;BIT&gt;

A:Cross-references: GB:U04740; NID:g470384; PIDN:AAA18422.1; PID:g470385

C:Superfamily: ATP receptor P2u

Query Match 20.4%; Score 362; DB 2; Length 341;

Best Local Similarity 28.9%; Pred. No. 8.8e-24;

Matches 96; Conservative 66; Mismatches 120; Indels 50; Gaps 10;

Qy 20 DYKITQVLFPLLYTVLFFVGLITNGLAMRIF--FQIRSKSNFIIFLKNVTVIDLLMILT 76

Db 10 DSEFRYTLFPIVYGVIFILGVVANGYVILWVFNLYPSKLNKIKIFWNLTMADLLFLIT 69

Qy 77 PPKILSDAKLGTGPTLFTVCQVTSVIFYFTMYISIFLGLITIDRYOKTRPFTSNPK 136

Db 70 LPLMIVYYNEGDWILFNLCNAGCLFFINTYCSVAFLGVITYNRYQAVAYPIKTAQAT 129

Qy 137 NLLGAKILSVVWAFM-----FILSLPNMILTNRQPRDKNVKCSFLKSEFG--LWVHE 188

Db 130 TRKGISLSLIWISIVATASYFLATSTNVLPKOGSGNITRCFEHYEPYSVILVHV 189

Qy 177 FKSEFGIWMHEIVNYICQVIFWNLFIIVCYTLITKELYSYVTRGVGVKPRKKNV 236

Db 190 FITSCFFLVFF-----LIFYCNMVI--HTLLTRP-----VROQRKPEVKKRALWM 233

Qy 237 KVFIIVAFETCFVPEFHPIRYITLSQTRDVFDCATENTLFVVKESTLWLTSLNACLDPE 296

Db 234 -VCTVIAVFCVPHVWVQDFWTLAELG--YQTFHQAINDAHQITLCLSTNCVLDPIV 290

Qy 297 IYFFLCKSFN-----SLISMLKCPNSATS 321

Db 291 IYCFLTCKFRKHLSEKFKYSMRSRKC-SRATS 321

RESULT 6

I50241

G protein-coupled receptor 6H1 - chicken

N/Alternate names: purinoceptor 6H1

C:Species: Gallus gallus (chicken)

C&gt;Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 02-Jun-2000

C:Accession: I50241; JC4618

R:Kaplan, M.H.; Smith, D.I.; Sundick, R.S.

J. Immunol. 151, 628-636, 1993

A:Title: Identification of a G protein coupled receptor induced in activated T cells.

A:Reference number: I50241; MUID:93329058; PMID:8393036

A:Accession: I50241

A&gt;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-308 &lt;AP&gt;

A:Cross-references: GB:L06109; NID:g304383; PIDN:AAB05587.1; PID:g304384

R:Webb, T.E.; Kaplan, M.G.; Barnard, E.A.

Biochem. Biophys. Res. Commun. 219, 105-110, 1996

A:Title: Identification of 6H1 as a P2Y purinoceptor: P2Y5.

A:Reference number: JC4618; MUID:96190677; PMID:8619790

A:Accession: JC4618

A:Molecule type: mRNA

A:Residues: 1-308 &lt;WEB&gt;

A:Cross-references: GB:L06109; NID:g304383; PIDN:AAB05587.1; PID:g304384

A:Experimental source: T-cells

C:Comment: This receptor plays a role in T-cell activation.

C:Genetics:

A:Gene: P2Y5

C:Superfamily: ATP receptor P2u

C:Keywords: G protein-coupled receptor; transmembrane protein

F15-40/Domain: transmembrane #status predicted &lt;TM1&gt;

F151-74/Domain: transmembrane #status predicted &lt;TM2&gt;

F189-109/Domain: transmembrane #status predicted &lt;TM3&gt;

F133-153/Domain: transmembrane #status predicted &lt;TM4&gt;

F177-201/Domain: transmembrane #status predicted &lt;TM5&gt;

F227-248/Domain: transmembrane #status predicted &lt;TM6&gt;

F269-292/Domain: transmembrane #status predicted &lt;TM7&gt;

Query Match 20.1%; Score 357.5; DB 2; Length 308;

Best Local Similarity 29.5%; Pred. No. 1.9e-23;

Matches 87; Conservative 68; Mismatches 125; Indels 15; Gaps 8;

Qy 14 TSLCTRDYKIKTVLPFLYTVLFFVGLITNGLAMRIF--FQIRSKSNFIIFLKNVTVIDLL 72

Db 3 SSNCSTEDSFYKTLGYGVFVSVFVGLIANCAVIFFTLUKVRNETTMMNLAIISDLL 62

Qy 73 MLTTPFFKILSDAKLGTGPTLFTVCQVTSVIFYFTMYISIFLGLITIDRYOKTRPFT 132

Db 63 FVFTLPFIYFV-VRNWPPGVDLVCKISVTLFYTNMYGSIILFLACISVDRLAIVHPFRS 121

Qy 133 SNPKNLLGAKILSVVWAFMFLSLDPNML--TNRQPRDKNVKCSFLKSEFGIWMHE 188

Db 122 KTLRKNARIVCVAVWITVLAGSTPASFFPOSTNRQ-NTEQRTCPENFPESTWKTYSR 180  
 QY 189 IVNYICQVIFWINFLIVCYVTLTKELYSYVTRGVKPRKKNVKKVFIILIAVFFIC 248  
 Db 181 IVIFIEIVGFPIILINVTCTMTWRLINKPLTSR--NKLSKKKVLKMFVHLVIFPCF 238  
 QY 249 FVPHFARIPYTLQTRDVFDC--TAENTLFYVKESTLMTSLNACLDPFIYFF 300  
 Db 239 FVPINITILYSMLRTQWINCNSVVTAVRTIPV---TLCIAVSNCCDFPIYIF 290

RESULT 7  
 S15403  
 angiotensin II receptor type 1 - bovine  
 C:Species: Bos primigenius indicus x Bos primigenius taurus (cattle)  
 C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 24-Nov-1999  
 R:Accession: S15403  
 R:Saeki, K.; Yamano, Y.; Bardhan, S.; Iwai, N.; Murray, J.J.; Hasegawa, M.; Matsuda, Y.  
 Nature 351, 230-233, 1991  
 A:Title: Cloning and expression of a complementary DNA encoding a bovine adrenal angiotensin II receptor type 1  
 A:Reference number: S15403; MUID:91251900; PMID:2041569  
 A:Accession: S15403  
 A:Status: Preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <RES>  
 A:Cross-references: GB:X62294; NID:g43; PIDN:CAAA44182.1; PID:g44  
 C:Superfamily: vertebrate rhodopsin

Query Match 19.1%; Score 339; DB 2; Length 359;  
 Best Local Similarity 27.9%; Pred. No. 9e-22; Mismatches 143; Indels 40; Gaps 10;  
 Matches 95; Conservative 62

QY 26 VLFPFLYTLVFPVGLITNGL-AMRIFFQIRSKSNFIIFLKNVTISDLMLITLTPFKILSD 84  
 Db 29 IMIPTLYSIIFVVGIFGNSLVVIVFYFMKLTAVSVFLLNALADLCFLTLPLWAVYT 88  
 QY 85 AKLGTGPLETFVVCQVTSVIFFTWYISIFLGLITIDRYOKTTPFKTSNPKLLGAKIL 144  
 Db 89 AMEYRWPFNGYLCKTASASVSNLYASVFLTCLSIDRYLAIVHPMKSRRLRTMLVAVT 148  
 QY 145 SVVIAFWAFLLSLPNMILT-NRQPRDKNKKCSF-----LKSEFGLVWHEIVNYICQ 195  
 Db 149 CIIIMLLAGLASLPPIIHRNVFFIENTNITVCAFYHESQNSTLPVGLGT-KNILGFL-- 205  
 QY 196 VIFWNLFLIVCYTLTKELYSYVTRGVKPRKKNVKKVFIILIAVFFICFVPHFA 255  
 Db 206 ----FPFLIILTSYTLWKLKAYEIQK--NKPRKDDIFKIILAIPLVFPF-----FS 252  
 QY 256 RPYTLQTRDVF-----DCTAENTLFYVKESTLMTSLNACLDPFIYFFLCKSPRNS 308  
 Db 253 WPHQIFTFMVDVLQGLIRDCKIEDIVDTAMPITICLAYFNCLNPLFYGLGKFKKY 312  
 QY 309 LISMLK-CPNSATSLSQNRK-----KEQGGGPNNEETP 341  
 Db 313 FLQLLKYPKAKSHSNLSKMTSLSYRSPENGNSSTKKP 352

RESULT 8  
 T09508  
 intron 17 purinergic receptor P2Y5 - human  
 N:Alternate names: G-protein coupled receptor  
 C:Species: Homo sapiens (man)  
 C:Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 24-Nov-1999  
 R:Accession: T09508  
 R:Bohm, S.K.; Trumpp, A.; Khatin, L.M.; Kong, W.; Pavan, D.G.; Bunnett, N.W.  
 submitted to the EMBL Data Library, April 1997  
 A:Description: The human purinergic receptor P2Y5 is encoded in intron 17 of the retinoblastoma gene  
 A:Reference number: Z16705  
 A:Accession: T09508  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-344 <BOH>

A:Cross-references: EMBL:AF000546; NID:g2232068; PID:g2232069  
 C:Genetics:  
 A:Map position: 13  
 C:Superfamily: ATP receptor P2u  
 C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 19.0%; Score 338; DB 2; Length 344;  
 Best Local Similarity 26.4%; Pred. No. 1.1e-21; Mismatches 146; Indels 18; Gaps 8;  
 Matches 87; Conservative 79

QY 13 NTSCLTRYKIKTQVLPFLYTLVFPVGLITNGLAMRIFF-QIRSKSNFIIFLKNVTISDL 71  
 Db 5 NSSHCFYNDSPKTYLTCGFMVFLGVSNCVAIYFICVLKVRNETTTTMINLAWSDL 64  
 QY 72 LMILTFPEFKILSDAKLGTGPLETFVVCQVTSVIFFTWYISIFLGLITIDRYOKTTPFK 131  
 Db 65 LEVFTLPIRIFY-FTRRWPFGLDLCKLSVLMFTNMYGSLFLTCLISVDRLAIVVFPK 123  
 QY 132 TSNPKLLGAKILSVIIFWAFNPLSLPNMILTNRQPRDKNKKC---SFLKSEFGLVWHE 188  
 Db 124 SKTLTKENAKIVCTGWLTVIGGSAPAVFVQSTHSQNNASEACFENFPEATWKTYSR 183  
 QY 189 IVNYICQVIFWINFLIVCYVTLTKELYSYVTRGVKPRKKNVKKVFIILIAVFFIC 248  
 Db 184 IVIFIEIVGFPIILINVTCTMTWRLINKPLTSR--SKINKTKVLKMFVHLIIFCFC 241  
 QY 249 FVPHFARIPYTLQTRDVFDC--TAENTLFYVKESTLMTSLNACLDPFIYFFLCKSF 305  
 Db 242 FVPYNINILYSLVTRQTFVNCVVAAVRTWYPI---TLCIAVSNCCDFPIYVFTSDTI 298  
 QY 306 RNSLSMLKCPNSATSLSQNRKKEQGGD 335  
 Db 299 QNS-----IMKNQSVRRS-DFRFSEVHGAE 323

RESULT 9  
 I39418  
 angiotensin II receptor type 1b - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 24-Nov-1999  
 R:Accession: I39418  
 R:Kuroda, S.  
 Biochem. Biophys. Res. Commun. 199, 467-474, 1994  
 A:Title: Novel subtype of human angiotensin II type 1 receptor: cDNA cloning and expression  
 A:Reference number: I39418; MUID:94183213; PMID:8135787  
 A:Accession: I39418  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-359 <RES>  
 A:Cross-references: GB:D13814; NID:g471120; PIDN:BAA02968.1; PID:g471121  
 C:Superfamily: vertebrate rhodopsin

Query Match 18.5%; Score 329; DB 2; Length 359;  
 Best Local Similarity 28.7%; Pred. No. 6.6e-21; Mismatches 137; Indels 34; Gaps 9;  
 Matches 92; Conservative 58

QY 26 VLFPFLYTLVFPVGLITNGL-AMRIFFQIRSKSNFIIFLKNVTISDLMLITLTPFKILSD 84  
 Db 29 VMIPTLYSIIFVVGIFGNSLVVIVFYFMKLTAVSVFLLNALADLCFLTLPLWAVYT 88  
 QY 85 AKLGTGPLETFVVCQVTSVIFFTWYISIFLGLITIDRYOKTTPFKTSNPKLLGAKIL 144  
 Db 89 AMEYRWPFNGYLCKTASASVSNLYASVFLTCLSIDRYLAIVHPMKSRRLRTMLVAVT 148  
 QY 145 SVVIAFWAFLLSLPNMILT-NRQPRDKNKKCSF-----LKSEFGLVWHEIVNYICQ 195  
 Db 149 CIIIMLLAGLASLPPIIHRNVFFIENTNITVCAFYHESRNSLPIGLGLTKNILGS--C- 205  
 QY 196 VIFWNLFLIVCYTLTKELYSYVTRGVKPRKKNVKKVFIILIAVFFICFVPHFA 255  
 Db 206 ----FPFLIILTSYTLWKLKAYEIQK--NNPRNDIDIFRIIMAVLVPF-----FS 252  
 QY 256 RPYTLQTRDVF-----DCTAENTLFYVKESTLMTSLNACLDPFIYFFLCKSPRNS 308

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Db 253 WIPQIFTFDLVLIQQIIRDCRIADIVDTAMPITIIWAFNNCLNPLFYGLGKFKKD 312
QY 309 LISMLK-CPNSATSLSQDNRK 328
Db 313 ILQLKVIIPPKAKSHSNLSLK 333

RESULT 10
S44425
angiotensin II receptor type 1 - dog
C:Species: Canis lupus familiaris (dog)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999
C:Accession: S44425
R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L.
FEBS Lett. 343, 146-150, 1994
A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor
A:Reference number: S44425; MUID:94222186; PMID:8168620
A:Accession: S44425
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-359 <BUR>
A:Cross-references: PIDN:AA830674.1; PID:G546569
A:Experimental source: liver
A:Superfamily: vertebrate rhodopsin

Query Match 18.3%; Score 326; DB 2; Length 359;
Best Local Similarity 29.2%; Pred. No. 1.2e-20;
Matches 92; Conservative 54; Mismatches 147; Indels 22; Gaps 8;

QY 26 VLPFLLYTVLFFVGLIINGLA-MRIFQIRKSNFIIFLKNVTIVISDLMLITPPFKILSD 84
Db 29 VMIEPTLYSIIFVVGIFGNSLAVIIVFYFMKLTIVASVFLNLALADLCFLTLPLWAVYT 88
QY 85 AKLGTGLRTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLGAKIL 144
Db 89 AMEYRWPFNGYLVCKIASASVFNLYASVFLTCLSIDRYAVIIVHPKSPVRITMLAKVT 148
QY 145 SVVIWAFMFLSLPNNILTN-RQPRDNKKVCSF-----LKSEFGLVWHEIVNYICQ 195
Db 149 CIIWLLAGLASLPAIIHRNVFFIENTNITVCAPHYESQNSTLPIGLGLT-KNIIGLF-- 205
QY 196 VIFWNLIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFRCFVPEHF 254
Db 206 ----FPFLIILTSYLLWKLKRAYEQK---NKPRNDIDFKIIMAVLFFFSWVPHQI 258
QY 255 ARIPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSMLK 314
Db 259 FTFLDLVLIQLGIHDCRIADIVDTAMPITICIAVFNNCLNPLFYGLGKFKKYFLQLLK 318
QY 315 -CPNSATSLSQDNRK 328
Db 319 YIPPKAKSHSNLSLK 333

RESULT 11
148705
proteinase activated receptor 2 - mouse
C:Species: Mus musculus (house mouse)
C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C:Accession: 148705
R:Nystedt, S.; Larsson, A.K.; Aberg, H.; Sundelin, J.
J. Biol. Chem. 270, 5950-5955, 1995
A:Title: The mouse proteinase-activated receptor-2 cDNA and gene. Molecular cloning and
A:Reference number: 148705; MUID:95197620; PMID:7890726
A:Accession: 148705
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-399 <RES>
A:Cross-references: EMBL:Z48043; NID:G663020; PIDN:CAA8097.1; PID:G663021
C:Superfamily: ATP receptor P2u

Query Match 18.3%; Score 325.5; DB 2; Length 399;
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Best Local Similarity 27.6%; Pred. No. 1.5e-20;
Matches 92; Conservative 73; Mismatches 141; Indels 27; Gaps 12;

QY 22 KITQVLPLLYTVLFFVGLIINGLA-MRIFQIRKSNFIIFLKNVTIVISDLMLITPPFK 80
Db 74 KLTIVFLPVVYIIVFVIGLPSGNALWIFLFRTRKKGPAVIYMANLALADLSVWPEFLK 133
QY 81 ILSDAKLGTPGLRTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLG 140
Db 134 ISYHLGNWYVYGEALCKVLIGFYGNMYCSILFMTCLSVQRYWVIYNPM--GHPKKAN 191
QY 141 AKI-LSVVIWAFMFLSLPNNIL--TNKQPRDNKKVCSFGLVWHEIVNYICQV- 196
Db 192 IAVGVSALAILWLLIFLVPIFYVMQTIYIFA-LNITTCVDVLPVLEV-GDMFNYFLSLA 249
QY 197 --IWFNFIIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFRCFVPEHF 254
Db 250 IGVFLFPALLTASAYVLMIKLTRSSANDHESEK--RQRAIRLIITVLAIFYCFAFSNL 307
QY 255 AR-IPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSML 313
Db 308 LLVVHYFLIKTQ-----RQSHVVALVIVLVALCLSTLNSCIDPFVYVYVSKDFRDHARNAL 361
QY 314 KCPNSAT-----SLSQDNKKKQDQGDPEET 340
Db 362 LCRSVRTVNRMQISLS-SNKFSKSGSYSSST 393

RESULT 12
148857
angiotensin II receptor type 1 - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 08-Oct-1999
C:Accession: 148857
R:Burns, K.D.; Inagami, T.; Harris, R.C.
Am. J. Physiol. 264, F645-F654, 1993
A:Title: Cloning of a rabbit kidney cortex AT1 angiotensin II receptor that is present
A:Reference number: 148857; MUID:93236091; PMID:7916579
A:Accession: 148857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:G299614; PIDN:AA826239.1; PID:G299615
A:Experimental source: proximal tubule cells
A>Note: sequence extracted from NCBI Backbone (NCBIN:129600, NCBI:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 18.3%; Score 325; DB 2; Length 359;
Best Local Similarity 29.2%; Pred. No. 1.5e-20;
Matches 92; Conservative 55; Mismatches 146; Indels 22; Gaps 8;

QY 26 VLPFLLYTVLFFVGLIINGLA-MRIFQIRKSNFIIFLKNVTIVISDLMLITPPFKILSD 84
Db 29 VMIEPTLYSIIFVVGIFGNSLAVIIVFYFMKLTIVASVFLNLALADLCFLTLPLWAVYT 88
QY 85 AKLGTGLRTFVCOVTSVIFVFTWYISISFLGLITIDRYOKTTRPKTSNPKNLGAKIL 144
Db 89 AMEYRWPFNGYLVCKIASASVFNLYASVFLTCLSIDRYAVIIVHPKSPVRITMLAKVT 148
QY 145 SVVIWAFMFLSLPNNILTN-RQPRDNKKVCSF-----LKSEFGLVWHEIVNYICQ 195
Db 149 CIIWLLAGLASLPAIIHRNVFFIENTNITVCAPHYESQNSTLPIGLGLT-KNIIGLF-- 205
QY 196 VIFWNLIVIVCVTLTKELYSYVTRGVGKVPKKNVKVFI-IIAVFRCFVPEHF 254
Db 206 ----FPFLIILTSYLLWKLKRAYEQK---NKPRNDIDFKIIMAVLFFFSWVPHQI 258
QY 255 ARIPYTLSTQTRDVEDCTAENTLFYVKESTLWLTSLNACLDPFIYFFLCKSFNLSMLK 314
Db 259 FTFLDLVLIQLGIHDCRIADIVDTAMPITICIAVFNNCLNPLFYGLGKFKKYFLQLLK 318
QY 315 -CPNSATSLSQDNRK 328
```





Search completed: February 4, 2004, 14:30:59  
Job time : 21 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 4, 2004, 14:23:36 ; Search time 17 Seconds  
(without alignments)  
946.067 Million cell updates/sec

Title: US-09-780-576-2

Perfect score: 1778

Sequence: 1 MQAVDNLTSAPGNTSLCTRD.....SQDNRRKKEODGDPNEETPM 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1778	100.0	342	1 P2YC HUMAN	Q9h244 homo sapien
2	1748	98.3	342	1 P2YC MACFA	Q95kc3 macaca fasc
3	1555.5	87.5	347	1 P2YC MOUSE	Q9cpv9 mus musculus
4	1528.5	86.0	343	1 P2YC RAT	Q9epx4 rattus norv
5	772	43.4	338	1 P2YX HUMAN	Q15391 homo sapien
6	741.5	41.7	338	1 P2YX MOUSE	Q9esg6 mus musculus
7	694	39.0	305	1 P2YX RAT	Q35881 rattus norv
8	488	27.4	319	1 H963 HUMAN	Q14626 homo sapien
9	411.5	23.1	375	1 GP34 MOUSE	Q9xrk6 mus musculus
10	409.5	23.0	381	1 GP34 HUMAN	Q9upc5 homo sapien
11	394	22.2	342	1 PAFR HUMAN	P25105 homo sapien
12	382.5	22.1	342	1 PAFR CAVPO	P21556 cavia porce
13	379.5	21.3	361	1 EB12 HUMAN	P32249 homo sapien
14	367	20.6	345	1 CLT2 FIG	Q95n03 sus scrofa
15	366	20.6	341	1 PAFR RAT	Q62035 mus musculus
16	362	20.4	341	1 PAFR RAT	P46002 rattus norv
17	357.5	20.1	308	1 P2Y5 CHICK	P32250 gallus gall
18	347.5	19.5	345	1 CLT2 HUMAN	Q9ns75 homo sapien
19	347.5	19.5	537	1 P2Y8 XENLA	P79928 xenopus lae
20	344	19.3	309	1 CLT2 MOUSE	Q92ba1 mus musculus
21	339.5	19.1	309	1 CLT2 RAT	Q924t9 rattus norv
22	339	19.1	359	1 AG2R BOVIN	P25104 bos taurus
23	338	19.0	344	1 P2Y5 HUMAN	P43657 homo sapien
24	334	18.8	359	1 AG2R SHEEP	O77590 ovis aries
25	334	18.8	367	1 GP17 HUMAN	Q13304 homo sapien
26	329	18.5	359	1 AG28 HUMAN	Q13725 homo sapien
27	328	18.4	340	1 CLT1 FIG	Q95n02 sus scrofa
28	327	18.4	359	1 AG2R FIG	P30555 sus scrofa
29	326	18.3	359	1 AG2R CANFA	P43240 canis fam1
30	325.5	18.3	399	1 PAR2 MOUSE	P55086 mus musculus
31	325	18.3	359	1 AG2R RABIT	P34976 oryctolagus
32	321	18.1	359	1 AG2R HUMAN	P30556 homo sapien
33	320	18.0	359	1 AG2R_CAVPO	Q9wv26 cavia porce

#### ALIGNMENTS

##### RESULT 1

ID	P2YC HUMAN	STANDARD;	PRT;	342 AA.
AC	Q9H244;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor) (P2Y(ADP))			
DE	(ADP-glucose receptor) (ADPG-R) (P2Y(AC)) (P2Y(cyc)) (P2T(AC))			
DE	(SPI999)			
GN	P2RY12 OR HORK3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21037966; PubMed=11196645;			
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,			
RA	Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,			
RA	Conley P.B.;			
RT	"Identification of the platelet ADP receptor targeted by			
RT	antithrombotic drugs";			
RL	Nature 403:202-207(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Hypothalamus;			
RX	MEDLINE=21269433; PubMed=11104774;			
RA	Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,			
RA	Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,			
RA	Monsma F.J. Jr.;			
RT	"ADP is the cognate ligand for the orphan G protein-coupled receptor			
RT	SP1999";			
RL	J. Biol. Chem. 276:8608-8615(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=21394281; PubMed=11502873;			
RA	Takasaki J., Kamchaya M., Saito T., Matsumoto M., Matsumoto S.-I.,			
RA	Ohishi T., Soga T., Matsushima H., Furuichi K.;			
RT	"Molecular cloning of the platelet P2T(AC) ADP receptor:			
RT	pharmacological comparison with another ADP receptor, the P2Y1			
RT	receptor.";			
RL	Mol. Pharmacol. 60:432-439(2001).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Reinscheid R.K., Notchacker H.-P., Wang Z., Zeng J., Ehler P.J.,			
RA	Civelli O.;			
RT	"ADP-glucose activates a G-protein coupled receptor and inhibits			
RT	smooth muscle contractions.";			
RL	Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;			
RT	"Identification of G protein-coupled receptor genes from the human			
RT	genome sequence.";			

34	320	18.0	370	1	P2Y9 HUMAN	Q99677 homo sapien
35	319.5	18.0	365	1	GP68 HUMAN	Q15743 homo sapien
36	319	17.9	359	1	AG2R RAT	P25095 rattus norv
37	319	17.9	359	1	AG2S RAT	P29089 rattus norv
38	318	17.9	359	1	AG2R MOUSE	P29754 mus musculus
39	318	17.9	361	1	P2Y4 MOUSE	Q9jjs7 mus musculus
40	315.5	17.8	398	1	OPRM RAT	P33535 rattus norv
41	316	17.8	359	1	AG2S MOUSE	P29755 mus musculus
42	316	17.8	377	1	APJ RAT	Q9jhg3 rattus norv
43	316	17.8	397	1	PAR2 RAT	Q63645 rattus norv
44	313.5	17.6	380	1	APJ HUMAN	P35414 homo sapien
45	313.5	17.6	401	1	OPRM FIG	Q95247 sus scrofa

Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

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RL  SEQUENCE FROM N.A.
RN  TISSUE=Prostate;
RC  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA  Datchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grinnwood J., Schmutz J., Myers R.M.,
RA  Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalley D.E.,
RA  Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT  "Generation and initial analysis of more than 15,000 full-length
RT  human and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
CC  -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC  inhibit the adenylyl cyclase second messenger system. Not
CC  activated by UDP and UTP. Involved in platelets aggregation.
CC  -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC  -!- TISSUE SPECIFICITY: Highly expressed in the platelets, lower
CC  levels in the brain. Lowest levels in the lung, appendix,
CC  pituitary and adrenal gland. Expressed in the spinal cord and in
CC  the fetal brain.
CC  -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; AF313449; AAG48944.1; -
DR  EMBL; AF321815; AAK00948.1; -
DR  EMBL; AB052684; BAB60824.1; -
DR  EMBL; AF310685; AAL3292.1; -
DR  EMBL; AB083596; BAB8309.1; -
DR  EMBL; BC017898; AAH17898.1; -
DR  Genew; HGNC:18124; P2RY12.
DR  MIM; 600515; -
DR  GO; GO:0007599; P:hemostasis; NAS.
DR  InterPro; IPR000276; GPCR_Rhodpsn.
DR  InterPro; IPR005394; P2Y12_putnreceptor.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCR_Rhodopsin.
DR  PRINTS; PR01569; P2Y12_P2Y12.
DR  PROSITE; PS00217; G_PROTEIN_RECEP_F1_1; FALSE_NEG.
DR  PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW  G-protein coupled receptor; Transmembrane; Glycoprotein.
FT  DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 26 46 1 (POTENTIAL).
FT  DOMAIN 47 58 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 59 79 2 (POTENTIAL).
FT  DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 100 120 3 (POTENTIAL).
FT  DOMAIN 121 142 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 143 163 4 (POTENTIAL).
FT  DOMAIN 164 191 EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM 192 212 5 (POTENTIAL).
FT  DOMAIN 213 233 CYTOPLASMIC (POTENTIAL).
FT  TRANSMEM 234 254 6 (POTENTIAL).
FT  DOMAIN 255 281 EXTRACELLULAR (POTENTIAL).

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FT  TRANSMEM 282 302 7 (POTENTIAL).
FT  DOMAIN 303 342 CYTOPLASMIC (POTENTIAL).
FT  BY SIMILARITY 175 BY SIMILARITY.
FT  CARBOHYD 97 6 N-LINKED (GLCNAC...) (POTENTIAL).
FT  CARBOHYD 13 13 N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 342 AA; 39438 MW; 8553D2746C89176D CRC64;

Query Match 100.0%; Score 1778; DB 1; Length 342;
Best Local Similarity 100.0%; Pred. No. 3.7e-117;
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQAVDNLSAPGNTSLCTRDYKIQVLPFLIYTVLFFVGLITNGLAMRPFQIRSKNFI 60
DB 1 MQAVDNLSAPGNTSLCTRDYKIQVLPFLIYTVLFFVGLITNGLAMRPFQIRSKNFI 60
QY 61 IFKNTVSDLLMLITPFPKILSDAKLTGRLTFVCOVTSVIFFTWYISIFLGLITI 120
DB 61 IFKNTVSDLLMLITPFPKILSDAKLTGRLTFVCOVTSVIFFTWYISIFLGLITI 120
QY 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFFWLLSNMILTNRPQDKXKVKCSFLKS 180
DB 121 DRYQKTRFPKTSNPKNLGAKILSVIWAFFWLLSNMILTNRPQDKXKVKCSFLKS 180
QY 181 EFGVLVHEIVNYICOVIFWNIPLIVICVYITLITKELYSYVTRGVGKVPKKNVKVFI 240
DB 181 EFGVLVHEIVNYICOVIFWNIPLIVICVYITLITKELYSYVTRGVGKVPKKNVKVFI 240
QY 241 IIAVFFICFVPHFARIPTYSQTRDVEDCTAENTLFVYKESITLWLTSLNACLOPFIYFF 300
DB 241 IIAVFFICFVPHFARIPTYSQTRDVEDCTAENTLFVYKESITLWLTSLNACLOPFIYFF 300
QY 301 LCKSFNLSIMLKPNSATSLSQDNRRKKEQGGDPNEETPM 342
DB 301 LCKSFNLSIMLKPNSATSLSQDNRRKKEQGGDPNEETPM 342

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## RESULT 2

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P2YC_MACFA
ID P2YC_MACFA STANDARD; PRT; 342 AA.
AC Q95KC3; Q95GT8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2RY12.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9541;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Frontal cortex, and Medulla oblongata;
RA Oeada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries.";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR  EMBL; AB056385; BAB33041.1; -

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DR EMBL; AB062981; BAB60747.1; -
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR02037; GPCR_Rhodopsin.
DR PRINTS; PR01569; P2Y12_PRNCPTR.
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; FALSE NEG.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 25 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 26 46 1 (POTENTIAL).
FT DOMAIN 47 58 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 59 79 2 (POTENTIAL).
FT DOMAIN 80 99 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 100 120 3 (POTENTIAL).
FT DOMAIN 121 142 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 143 163 4 (POTENTIAL).
FT DOMAIN 164 191 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 192 212 5 (POTENTIAL).
FT DOMAIN 213 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 6 (POTENTIAL).
FT DOMAIN 255 281 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 282 302 7 (POTENTIAL).
FT DOMAIN 303 342 CYTOPLASMIC (POTENTIAL).
FT DISULFID 97 175 BY SIMILARITY.
FT CARBOHYD 6 6 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 49 49 I -> T (IN REF. 1; BAB33041).
FT CONFLICT 89 89 A -> T (IN REF. 1; BAB33041).
SQ SEQUENCE 342 AA; 39479 MW; E93FC26BFF5EC4C CRC64;

Query Match 98.3%; Score 1748; DB 1; Length 342;
Best Local Similarity 98.0%; Pred. No. 4.5e-115;
Matches 335; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Cy 1 MQAVDNTSAPGNTSLCTRDYKTKITQVLPFLYTVLFPVGLITNGLNLRFFQIRSKNFI 60
Db 1 MQAIDNLTSPGNTSLCTRDYKTKITQVLPFLYTVLFPVGLITNGLNLRFFQIRSKNFI 60
Qy 61 IFLKNTVISDLMLTTPFKILSDAKLGTGTPFTVQNTSVIFFTWISIFLGLITI 120
Db 61 IFLKNTVISDLMLTTPFKILSDAKLGTGTPFTVQNTSVIFFTWISIFLGLITI 120
Qy 121 DRYQKTRPFTKSNPKNLGAKILSVVIVAFMFLSLPMLNLRPRDNKVKKCSFLKS 180
Db 121 DRYQKTRPFTKSNPKNLGAKILSVLIVAFMFLSLPMLNLRPRDNKVKKCSFLKS 180
Qy 181 EFGLVWHEIVNYICQVFWINFLIVICVYTLITKELYRSVTRTGKVPKKNVKKVFI 240
Db 181 EFGLVWHEIVNYICQVFWINFLIVICVYTLITKELYRSVTRTGKVPKKNVKKVFI 240
Qy 241 IIAVFFICFPFFHARIPYTLSDTRVDCTAENTLFFVKESTLWLTSLNACLDPIYFF 300
Db 241 IIAVFFICFPFFHARIPYTLSDTRVDCTAENTLFFVKESTLWLTSLNACLDPIYFF 300
Qy 301 LCKSFRNSLSMLKCPNSATSLQDNKKKQDGDGDPNEETPM 342
Db 301 LCKSFRNSLSMLKCPNSATSLQDNKKKQDGDGDPNEETPM 342

```

## RESULT 3

```

P2YC MOUSE
ID _P2YC_MOUSE STANDARD; PRT; 347 AA.
AC Q9CFV9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12).
GN P2Y12
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;

```

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RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J; TISSUE=Hippocampus, and Testis;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauber F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
[2]
RN SEQUENCE FROM N.A.
RP MEDLINE=2238257; PubMed=12477932;
RX Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wolny K.C., Hale S., Garcia A.M., Gay L.J., Rulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield J.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC -----
CC EMBL; AK013804; BAB29000.1; -
CC EMBL; AK014807; BAB29561.1; -
CC EMBL; BC025428; AAB25428.1; -
CC EMBL; BC027381; AAB27381.1; -
CC MGD; MGI:1918089; P2Y12.
CC GO; GO:0005887; C: integral to plasma membrane; IC.
CC GO; GO:0001609; F: adenosine receptor, G-protein coupled activity; IMP.
CC GO; GO:0001621; F: platelet ADP receptor activity; IMP.
CC GO; GO:0007188; P: G-protein signaling, coupled to cAMP nucleo. .; IMP.
CC GO; GO:0030188; P: platelet activation; IMP.
CC InterPro; IPR000276; GPCR_Rhodopsin.
CC InterPro; IPR005394; P2Y12_purinocptor.

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DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01569; P2Y12PRNCPT.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 126 3 (POTENTIAL).
FT DOMAIN 127 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 5 (POTENTIAL).
FT DOMAIN 219 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 347 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 181 BY SIMILARITY.
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 3 V -> M (IN REF. 2; AAH25428).
SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;

Query Match 87.5%; Score 1555.5; DB 1; Length 347;
Best Local Similarity 88.7%; Pred. No. 1.1e-101; Indels 1; Gaps 1;
Matches 299; Conservative 16; Mismatches 21;

QY 6 NLTSAPGNISLCTRDYKIQVLFFLLVTLVFFVGLITNGLAMRIFFQIRKSNFIIFLKN 65
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 NTSIPGSLTCDYKIQVLFFLLVTLVFFVGLITNGLAMRIFFQIRKSNFIIFLKN 71
QY 66 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 125
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
72 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYLK 131
QY 126 TTRPFTSNPNKLLGAKILSVIWAFLSLPNNILTNQPRDKNVKCSFLKSEFGLV 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 TTRPFTSSPNLLGAKILSVIWAFLSLPNNILTNRRPKDKVTKCSFLKSEFGLV 191
QY 186 WHEIYNYICQVIFNFIIVICVTLTKELYRSYVTRGVKPRKKNVKKVFIIAVF 245
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
192 WHEIYNYICQVIFNFIIVICVSLTKELYRSYVTRGSAPKPKRVKIVKFIIAVF 251
QY 246 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 305
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
252 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 311

RESULT 4
P2YC_RAT
ID P2YC_RAT STANDARD; PRT; 343 AA.
AC Q9EPX4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE P2Y purinoceptor 12 (P2Y12) (P2Y12 platelet ADP receptor).
GN P2Y12.
CS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RX [1]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley;
MEDLINE=21037966; PubMed=11196645;

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RA RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RT "Identification of the platelet ADP receptor targeted by
RT antithrombotic drugs.";
RL Nature 409:202-207(2001).
CC -!- FUNCTION: Receptor for ADP and ATP coupled to G-proteins that
CC inhibit the adenylyl cyclase second messenger system (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF313450; AAG48945.1;
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR InterPro; IPR005394; P2Y12_purinocptor.
DR Pfam; PF00001; 7tm1; 1.
DR PRINTS; PR00237; GPCRHHODOPSN.
DR PRINTS; PR01569; P2Y12PRNCPT.
DR PROSITE; PS00237; G-PROTEIN RECP F1_1; FALSE_NEG.
DR PROSITE; PS00262; G-PROTEIN RECP F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 52 1 (POTENTIAL).
FT DOMAIN 53 64 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 65 85 2 (POTENTIAL).
FT DOMAIN 86 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 126 3 (POTENTIAL).
FT DOMAIN 127 148 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 149 169 4 (POTENTIAL).
FT DOMAIN 170 197 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 198 218 5 (POTENTIAL).
FT DOMAIN 219 239 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 240 260 6 (POTENTIAL).
FT DOMAIN 261 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 308 7 (POTENTIAL).
FT DOMAIN 309 343 CYTOPLASMIC (POTENTIAL).
FT DISULFID 103 181 BY SIMILARITY.
FT CARBOHYD 7 7 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 12 12 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 3 3 V -> M (IN REF. 2; AAH25428).
SQ SEQUENCE 343 AA; 39047 MW; 7AEOAFCE6674136 CRC64;

Query Match 86.0%; Score 1528.5; DB 1; Length 343;
Best Local Similarity 86.9%; Pred. No. 8.6e-100; Indels 5; Gaps 1;
Matches 293; Conservative 17; Mismatches 22;

QY 6 NLTSAPGNISLCTRDYKIQVLFFLLVTLVFFVGLITNGLAMRIFFQIRKSNFIIFLKN 65
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
12 NTSIPGSLTCDYKIQVLFFLLVTLVFFVGLITNGLAMRIFFQIRKSNFIIFLKN 71
QY 66 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYOK 125
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
72 TVISDLMLFPFKILSDAKLGTGPLRTFVQVTSVIFFTWYISIFGLITIDRYLK 131
QY 126 TTRPFTSNPNKLLGAKILSVIWAFLSLPNNILTNQPRDKNVKCSFLKSEFGLV 185
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
132 TTRPFTSSPNLLGAKILSVIWAFLSLPNNILTNRRPKDKVTKCSFLKSEFGLV 191
QY 186 WHEIYNYICQVIFNFIIVICVTLTKELYRSYVTRGVKPRKKNVKKVFIIAVF 245
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
192 WHEIYNYICQVIFNFIIVICVSLTKELYRSYVTRGSAPKPKRVKIVKFIIAVF 251
QY 246 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 305
DB : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
252 FICFVPPHFAIPYTLSTQTRVDFDCTAENTLFYVKESTLWLTSLNACLDPPFIYFLCKSF 311

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306 RNSLISMLKCPNSATSLSQDNRRKKQGGDPNSETPM 343
312 RNSLISMLKCPNSATSLSQDNRRKKQGGDPNSETPM 343
312 RNSLISMLKCPNSATSLSQDNRRKKQGGDPNSETPM 343

RESULT 5
P2YX_HUMAN
IID P2YX_HUMAN STANDARD; PRT; 338 AA.
AC Q15391;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE UDP-glucose receptor (G protein-coupled receptor GPR105 or KIAA0001).
GN GPR105 OR KIAA0001.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; NCBI_TaxId=9606;
OX [1]
PC TISSUE=Bone marrow;
RP SEQUENCE FROM N.A.
RX MEDLINE=96051387; PubMed=7584026;
RA Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawasato S., Nagase T., Seki N., Ishikawa K.-I., Tabatake T.
RT "Prediction of the coding sequences of unidentified cDNA clones from a human cell line KG-1."
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) were identified from human cell line KG-1."
RT analysis of randomly sampled cDNA clones from human cell line KG-1."
RT cell line KG-1."
RT DNA Res. 1:27-35(1994).
RT [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21426338; PubMed=11524702;
RA Joensuu T., Haemäläinen R., Yuan B., Johnson C., Gasparini P., Zelante L., Pirvola U., Pakarinen L., de la Chapelle A., Sankila E.-M.;
RT "Mutations in a novel gene with transmembrane domain syndrome type 3."
RT Am. J. Hum. Genet. 69:673-684(2001).
RT [3]
RP FUNCTION.
RX MEDLINE=20219108; PubMed=10753868;
RA Chambers J.K., MacDonald L.E., Sarau H.M., Ames R.A., Foley J.J., Zhu Y., McLaughlin M.M., Murdock P., M. Trill J., Swift A., Aiyar N., Taylor P., Vawter L., Szekeres P., Hervieu G., Scott C., Watson J.M., M. Klein C., Bergsma D.J., Wilson S., Livi G.P.;
RT "A G protein-coupled receptor for UDP-glucose."
RT J. Biol. Chem. 275:10767-10771(2000).
RX MEDLINE=20219108; PubMed=10753868;
RA Chambers J.K., MacDonald L.E., Sarau H.M., Ames R.A., Foley J.J., Zhu Y., McLaughlin M.M., Murdock P., M. Trill J., Swift A., Aiyar N., Taylor P., Vawter L., Szekeres P., Hervieu G., Scott C., Watson J.M., M. Klein C., Bergsma D.J., Wilson S., Livi G.P.;
RT "A G protein-coupled receptor for UDP-glucose."
RT J. Biol. Chem. 275:10767-10771(2000).
CC -!- FUNCTION: Receptor for UDP-glucose and other U- G-proteins. Not activated by ATP, ADP, UTP or
CC -!- SUBCELLULAR LOCATION: Integral membrane protein
CC -!- TISSUE SPECIFICITY: Highest expression in the tissue, stomach and intestine, intermediate levels in spleen, lung and heart, lowest levels in the kidney.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLERS.
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CC or send an email to license@ebi.ac.uk.
CC -----
CC EMBL: D13626; AAA02791.1;
CC EMBL: AF456925; BAA47764.1;
CC GO: GN0116021; C: integral to membrane; NAS,
CC GO: GO:0045029; F: UDP-activated nucleotide receptor
CC GO: GO:0007186; P: G-protein coupled receptor protein
CC InterPro: IPR000276; GPCR Rhodopsin.
CC InterPro: IPR005466; UDPG Receptor.
CC Pfam: PF00001; 7tm 1.
CC -----

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DR	PRINTS; PRO0237; GPCRHHOOPGN.
DR	PRINTS; PRO1655; UDPGLUCOSER.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR F1.1; FALSE_NEG.
DR	PROSITE; PS00237; G PROTEIN RECEPTOR F1.2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.
FT	DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 30 50 1 (POTENTIAL).
FT	DOMAIN 51 55 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 56 76 2 (POTENTIAL).
FT	DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 97 117 3 (POTENTIAL).
FT	DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 140 160 4 (POTENTIAL).
FT	DOMAIN 161 188 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 189 209 5 (POTENTIAL).
FT	DOMAIN 210 234 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 235 255 6 (POTENTIAL).
FT	DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 279 299 7 (POTENTIAL).
FT	DOMAIN 300 338 CYTOPLASMIC (POTENTIAL).
FT	DISULFID 94 172 BY SIMILARITY.
FT	CARBOHYD 3 3 N-LINKED (GLCNAC... ) (POTENTIAL).
FT	CARBOHYD 161 161 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ	SEQUENCE 338 AA; 389971 MW; 8DBE7C782CB4753D CRC64;

  

Query Match		43.4%; Score 772; DB 1; Length 338;
Best Local Similarity		47.5%; Pred. No. 3.9e-47;
Matches 149; Conservative	60; Mismatches 105; Indels	0; Gaps 0;

  

QY	6	NLTSPAGNTSLCTRDYKKTQVLFPFLTYTLVFFVGLITNGLAMRIFFOIRSKSNPIIFLKN	65
DB	3	NSTSTQPPDESCQNLIITQQIIPLVYCMVFIAILINGVGWIFFVPSSKSPIIYLKN	62
QY	66	TIVSDLLMLTTPFKILSDAKLGRLPTPCOVTSVLFYFTWVISISFLGLITIDRYOK	125
DB	63	IIVADFMVSUTPFKILGDSGLGPQNLNVEFCRSAVLFVNMFVSVLPFGLSFDRIYK	122
QY	126	TTRPFKTNPKNILGAKILLSVTWAFMFLSLPNMLITNQPRDKNVKCSFLKSEFGLV	185
DB	123	IVKPLMTSFIOYSYSKLLSVVMMLMLLAIVENIITNQSAREVTQIKCIELKSELGRK	182
QY	186	WHIEVNYICOVIWFNIPLIIVVCYTILTKELYSYVTRGVGVKVRKKVNVKFIILAVF	245
DB	183	WHKASNYIFAIVFWELLIIVFYTAIKKFIFSHLKSSNSNSTVKCKSRNFISIVFVF	242
QY	246	FICFVFPFHARIPTYTSQTRDFVDCAENTLFVYKGESTLMTSLNACLDPFIYFFLOCKSF	305
DB	243	FVCVFVPHIARIPTYKSTEAHYSQCKEILRWMEKEFTLLSAANCLDPIIYFFLCQPF	302
QY	306	RNSLIIMLKCPNSA 319	
DB	303	REILCKXHLPLKA 316	

  

RESULT 6		PRT; 338 AA.
P2YY MOUSE	STANDARD;	
ID P2XX MOUSE		
AC Q9ESG6;		
DT 28-FEB-2003 (Rel. 41, Created)		
DT 28-FEB-2003 (Rel. 41, Last sequence update)		
DT 28-FEB-2003 (Rel. 41, Last annotation update)		
DE UDP-glucose receptor (G protein-coupled receptor GPR105).		
GN GPR105.		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.		
NCBI_TaxID=10090;		
RN [1]		
RP SEQUENCE FROM N.A.		
RA Lee B.C., Scadden D.T.:		
RT "7 transmembrane G protein coupled receptor from hematopoietic progenitors."		
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.		

306 RNSLISMLKCPNSATLSLSDNRKKKGQGGDPNEETPM 342  
|||||:  
312 RNSLMSMLRC-----STGANKKKKGEGGDPSEETPM 343

RESULT 5  
P2YX\_HUMAN  
ID P2YX\_HUMAN STANDARD; PRt; 338 AA.  
AC Q15391;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-FEB-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE UDP-glucose receptor (G protein-coupled receptor GPR105).  
GN GPR105 OR KIAA0001.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
RN SEQUENCE FROM N.A.  
RP TISSUE=Bone marrow;  
RC MEDLINE=96051387; PubMed=7584026;  
RX Nomura N., Miyajima N., Suzuki T., Tanaka A., Kawarabayashi Y.,  
RA Sato S., Nagase T., Seki N., Ishikawa K.-I., Tabata S.;  
RT "Prediction of the coding sequences of unidentified human genes. I.  
RT The coding sequences of 40 new genes (KIAA0001-KIAA0040) deduced by  
RT analysis of randomly sampled cDNA clones from human immature myeloid  
RT cell line KG-1";  
RL DNA Res. 1:27-35(1994).  
[2]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=21426338; PubMed=11524702;  
RX Joensuu T., Haemaelainen R., Yuan B., Johnson C., Tegelberg S.,  
RA Gasparini P., Zelante L., Pirvola U., Pakarinen L., Lehesjoki A.-E.,  
RA de la Chapelle A., Sankila E.-M.;  
RT "Mutations in a novel gene with transmembrane domains underlie Usher  
RT syndrome type 3.";  
RL Am. J. Hum. Genet. 69:673-684(2001).  
[3]  
RN FUNCTION.  
RP MEDLINE=20219108; PubMed=10753868;  
RX Chambers J.K., Macdonald L.E., Sarau H.M., Ames R.S., Freeman K.,  
RA Foley J.J., Zhu Y., McLaughlin M.M., Murdock P., McWilliam L.,  
RA Trill J., Swift A., Aliyar N., Taylor P., Vawter L., Naheed S.,  
RA Szekeres P., Hervaeu G., Scott C., Watson J.M., Murphy A.J., Duzic E.,  
RA Klein C., Bergama D.J., Wilson S., Livi G.P.;  
RT "A G protein-coupled receptor for UDP-glucose.";  
RL J. Biol. Chem. 275:10767-10771(2000).  
CC -!- FUNCTION: Receptor for UDP-glucose and other UDP-sugar coupled to  
CC G-proteins. Not activated by ATP, ADP, UTP or AMP.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
CC -!- TISSUE SPECIFICITY: Highest expression in the placenta, adipose  
CC tissue, stomach and intestine, intermediate levels in the brain,  
CC spleen, lung and heart, lowest levels in the kidney.  
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
CC  
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CC or send an email to licenses@isb-sib.ch).  
CC  
CC EMBL; DI3626; BAA02791.1; --  
CC EMBL; AF456925; AAL47764.1; --  
CC Gene; HGNC:16442; GPR105.  
DR GO: 0016021; C: integral to membrane; NAS.  
DR GO: 0045029; F: UDP-activated nucleotide receptor activity; NAS.  
DR GO: 0007186; P: G-protein coupled receptor protein signalin...; NAS.  
DR InterPro; IPRO00276; GPCR Rhodopsin.  
DR Pfam; PF00001; 7tm 1; 1.  
DR



```
QY 64 KNTVISDLMLTPPKILSDAKLGTGLRTFVQCVTSVIFYFTMYISISFLGLITIDRY 123
DB 61 KNIVVAFLMGLTEFPKVLSDSGLPQLAVFVRSAVIFYNNVSVISAFFGLISFDY 120
QY 124 QKTRPRTKSNPKNLGAKILSVVWAFMFLSLPNNMLTNRPDRDNKVKCKSFLKSEFG 183
DB 121 YKIVKPLLVSTQVSNYSKVLVWVLMILAVENIILTNQSVKDVNTQCMELKNELG 180
QY 184 LWHEIYNYICQVFWNLFIIVCYTLTKELVRSVVRTRGVKPKVNVKVERIIA 243
DB 181 RKWKASNYFVSVFWVFLTLTVFWAITRKFKSHLKRKNSISVKRKSRIISVL 240
QY 244 VFFICVFPFHARIPYTLQSDRVDFDCTAENTLFPYKESLWLTSLNACLDP 295
DB 241 AFVACFAPYHVARIPYTKSQTECHYSQAKETLLYTKFTLLSAAVCLDP 292

RESULT 8
H963_HUMAN STANDARD; PRT; 319 AA.
ID H963_HUMAN
AC O14626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor H963.
GN H963.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1].
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood monocytes;
RA MEDLINE=9903606; PubMed=9370294;
RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
RA Golden-Fleet K., Kelleher K., Kriz R., LaVallie E.R., Merberg D.,
RA Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
RT "A genetic selection for isolating cDNAs encoding secreted proteins.";
RL Gene 198:289-296(1997).
RN [2].
RP SEQUENCE FROM N.A.
RA MEDLINE=21426338; PubMed=11524702;
RA Joensuu T., Haemaelaeninen R., Yuan B., Johnson C., Tegelsberg S.,
RA Gasparini P., Zelante L., Pirvola U., Pakarinen L., Lehesjoki A.-E.,
RA de la Chapelle A., Sankila E.-M.;
RT "Mutations in a novel gene with transmembrane domains underlie Usher
RT syndrome type 3.";
RL Am. J. Hum. Genet. 69:673-684(2001).
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF002986; AAC51846.1; -
DR EMBL; AF411849; AAL47763.1; -
DR GO; GO:0016021; C: integral to membrane; NAS.
DR GO; GO:0007186; P: G-protein coupled receptor protein signalin. . .; NAS.
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHDOPSN
DR PROSITE; PS00237; G-PROTEIN RECEPTOR_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECEPTOR_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 42 1 (POTENTIAL).
```

```
FT DOMAIN 43 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 2 (POTENTIAL).
FT DOMAIN 70 89 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 90 110 3 (POTENTIAL).
FT DOMAIN 111 132 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 133 153 4 (POTENTIAL).
FT DOMAIN 154 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 202 5 (POTENTIAL).
FT DOMAIN 203 224 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 225 245 6 (POTENTIAL).
FT DOMAIN 246 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 289 7 (POTENTIAL).
FT DOMAIN 290 319 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 319 AA; 36754 MW; 7989821C10841114 CRC64;

Query Match 27.4%; Score 488; DB 1; Length 319;
Best Local Similarity 34.5%; Pred. No. 2.2e-27;
Matches 112; Conservative 62; Mismatches 125; Indels 26; Gaps 9;

QY 13 NTSCLTRDYKITQVLPFLLYTVLFFVGLITNGLAMRIFQIRSKSNFI-IFLKNTVISDL 71
DB 3 NSSFFCPVYKDEP-FTVFFYLVELVGIIGSCFATWAFIQKNTNHRVCVSIYLINLTADF 61
QY 72 LMILTFPEKILSDAKLGTGP--LRTEVCQVTSVIFYFTMYISISFLGLITIDRYQKTRP 129
DB 62 LTTALPVKIVVD--LGAPWKLIKIFHCQVACLIYNNMLSIIFLAFVSDRCLQLTHS 119
QY 130 FKTSNPKNLGAKILSVVWAFMFLSLPNNMLTNRPDRDNKVKCKSFLKSEFGSLVWHEI 189
DB 120 CKIVRIQBPFGAKMISTVWMLVLLIMVNNMIPKIDKEKSNVCGMEFKKEFGKRNWELL 179
QY 190 VNYICQVFWINE-LIVIVCVYTLTKELYSRYVYTRGVKVPK-KYNNKVFIILIAVFFI 247
DB 180 TNFICVAIP-LNFSAILILSNCLVIRQLYRN-----KONENYPNVKKALINLLVTTGII 234
QY 248 CFVPHFARIPTLSQSDRVDFDCTAENTLFPYKESLWLTSLNACLDPFYFFLCKSPFN 307
DB 235 CFVPHVIRIPTLSQSDREVITDCSTRISLFRKAKEATLLAVSNLCFDPILYHYLSKAFRS 294
QY 308 SLI-----SMLKCPNSA 319
DB 295 KVTETASPKEKTKAQKELRCENNA 319

RESULT 9
GP34_MOUSE STANDARD; PRT; 375 AA.
ID GP34_MOUSE
AC Q9RIK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1].
RP SEQUENCE FROM N.A.
RA MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
RA Schultz G., Gudermann T.;
RT "A novel subgroup of class I G-protein-coupled receptors.";
RL Biochim. Biophys. Acta 1446:57-70(1999).
CC -!- FUNCTION: ORPHAN RECEPTOR.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -!- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,  
 Lander E.S.,  
 Nat. Genet. 23:373-373 (1999).  
 CC FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM.  
 CC SUBCELLULAR LOCATION: Integral membrane protein.  
 CC SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; M80436; AAA60001.1; -  
 CC EMBL; M78674; AAA60002.1; -  
 CC EMBL; D10202; BAA01050.1; -  
 CC EMBL; M88177; AAA60214.1; -  
 CC EMBL; S52624; AAB24695.2; -  
 CC EMBL; L07334; AAA60108.1; -  
 CC EMBL; S56396; AAB25755.1; -  
 CC PIR; A40191; A40191  
 CC Genew; HGNC:9582; P1AFR.  
 CC MIM; 173393; -  
 CC GO; GO:0005887; C:integral to plasma membrane; TAS.  
 CC GO; GO:0004992; P:platelet activating factor receptor activity; TAS.  
 CC GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . . ; TAS.  
 CC GO; GO:0006935; P:chemotaxis; TAS.  
 CC GO; GO:0007186; P:G-protein coupled receptor protein signalin. . . ; TAS.  
 CC GO; GO:0006955; P:immune response; TAS.  
 CC GO; GO:0006954; P:inflammatory response; TAS.  
 CC GO; GO:0009405; P:phagocytosis; TAS.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm1.1.  
 CC PRINTS; PR00237; GPCRHOPOPSN.  
 CC PROSITE; PS00237; G-PROTEIN RECP\_F1\_1; 1.  
 CC PROSITE; PS00262; G-PROTEIN RECP\_F1\_2; 1.  
 CC G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;  
 CC Polymorphism.  
 KW Polymorphism.  
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 17 38 1 (POTENTIAL).  
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 55 74 2 (POTENTIAL).  
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 92 113 3 (POTENTIAL).  
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 134 155 4 (POTENTIAL).  
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 185 205 5 (POTENTIAL).  
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 234 254 6 (POTENTIAL).  
 FT TRANSMEM 255 276 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 277 296 7 (POTENTIAL).  
 FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 90 173 BY SIMILARITY.  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . . ) (POTENTIAL).  
 FT VARIANT 224 224 /FTIDVAR\_011851.  
 FT VARIANT 338 338 N -> S (IN dbSNP:5939).  
 FT VARIANT 338 338 /FTIDVAR\_011852.  
 FT CONFLICT 28 28 L -> P (IN REF. 6).  
 FT CONFLICT 66 66 F -> L (IN REF. 6).  
 FT CONFLICT 95 95 C -> R (IN REF. 6).  
 FT CONFLICT 227 228 KR -> TG (IN REF. 4).  
 FT CONFLICT 227 228 KR -> TT (IN REF. 6).  
 FT CONFLICT 247 247 P -> A (IN REF. 6).  
 FT CONFLICT 316 316 K -> N (IN REF. 5).

SQ SEQUENCE 342 AA; 39203 MW; 890073C9EBA79228 CRC64;  
 Query Match 22.2%; Score 394; DB 1; Length 342;  
 Best Local Similarity 32.6%; Pred. No. 8e-21;  
 Matches 107; Conservative 61; Mismatches 134; Indels 26; Gaps 10;  
 QY 11 PNTSLCTRDYKIVTQVLPPLLYTVLFFVGLTNGLAMRIPQIR--SKSNFI-IFLKNVY 67  
 DB 3 PHDSHMDSEPRYT--LPIIVYSIIFVLGVANGVLMVFARLYPCKKFKIEMVNL 60  
 QY 68 ISDLMLITFPFKILSDAKLGTPLRTFCVQVTSVIFVFTWYISIFLGLITIDRYQKTT 127  
 DB 61 MADMLFLITLPLWIVVYQGNWLPKELNVCAGCLFEINTYCSVAFGLVITYNRFQAVT 120  
 QY 128 RPKTSNPKNLGAKILSVIIVW----AFMFLLSPLMLNTNRPDK---NVKCSFLK 179  
 DB 121 REIKTAQANTRKRGISLSLVIWVAIVGAASYFLIDS---TNTVPDSAGSNVTRC-FEH 176  
 QY 180 SEFGLVWHEIVNYICQVFWINFLIVICVTLITKELVRSVVRGKVKPRKKNVAVF 239  
 DB 177 YEKGSVPVLIHIFVPSFFLVLLILFCNLVIRTLMLQPVQQQNAEVRRLMW-VC 235  
 QY 240 IIAVFFICFVFFHFAPIPTLSQTRVDCTAENTLKYKESLWLSNACLDPIFYF 299  
 DB 236 TVLAVFIIICFVPHVQVLPWTLAEI-GPQDSKFKQAINDAHQVTLICLLSTNCVLDPIVC 294  
 QY 300 FLCKSFN-----SLISMLKCPNSAT 320  
 DB 295 FLTKFKRHLEKFKYSMRSSKCSRAIT 322  
 RESULT 12  
 PAFR CAVPO STANDARD; PRT; 342 AA.  
 ID PAFR CAVPO  
 AC P21556;  
 DT 01-MAY-1991 (Rel. 18, Created)  
 DT 01-OCT-1991 (Rel. 19, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE Platelet activating factor receptor (PAF-R).  
 GN P1AFR.  
 OS Cavia porcellus (Guinea pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Caviidae; Cavia.  
 OC NCBI\_TaxID=10141;  
 RN [1]  
 SEQUENCE FROM N.A.  
 RP TISSUE=Lung;  
 RX MEDLINE=91101726; PubMed=1846231;  
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,  
 RA Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.  
 RT "Cloning by functional expression of platelet-activating factor  
 RL receptor from guinea-pig lung."  
 RL Nature 349:342-346 (1991).  
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC  
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-  
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS  
 CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-  
 CC CALCIUM SECOND MESSENGER SYSTEM.  
 CC SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.  
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 CC  
 CC EMBL; X56736; CAA40060.1; -  
 CC PIR; S13638; S13638.  
 CC InterPro; IPR000276; GPCR\_Rhodopsn.  
 CC Pfam; PF00001; 7tm1.1.

```
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein;
Chemoaxis.
FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 17 38 1 (POTENTIAL).
FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 55 74 2 (POTENTIAL).
FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 92 113 3 (POTENTIAL).
FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 134 155 4 (POTENTIAL).
FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 185 205 5 (POTENTIAL).
FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 234 254 6 (POTENTIAL).
FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 277 296 7 (POTENTIAL).
FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 4 4 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 169 169 N-LINKED (GLCNAC. .) (POTENTIAL).
FT DISULFID 90 173 BY SIMILARITY.
SQ SEQUENCE 342 AA; 38984 MW; B6413B3A5C87B175 CRC64;

Query Match 22.1%; Score 392.5; DB 1; Length 342;
Best Local Similarity 30.7%; Pred. No. 1e-20;
Matches 103; Conservative 66; Mismatches 146; Indels 21; Gaps 9;

QY 20 DYKTVQLFPLLYTVLVFVGLITGLAMRIFFQI--RSKSNFI-IFLKNVVISDLLMILT 76
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DSEPRYTLFPYVSIIFVGLIANGYVLPVARYPSKLEIKIFVNLTVADLLFLIT 69
QY 77 PPKILSDAKLGTGLRFLVFCQVTSVIFYFWYISIGFLGITIDRYOKTRPEKTSNPX 136
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DLPALVIVYSQGNWFLPFLCNLAGCLFFINTYCSVAFGLVITNRFQAVKPIKTAQAT 129
QY 137 NLLGAKILSVVIM-----AFWFLSLPMLITNQPRDKNVKCSFLKSEFG-----LVWH 187
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DTRKRGIALSLVIVAIAAASVFLVMDSTNVVSNKAGSGNITRC-FEHEYKSGKPVLIH 188
QY 188 EIVNYICOVI-FWNLFLVIVCYTLITKELVRSYVRGVGVKPKVNVKVFILIAVFP 246
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D189 -----ICVLGFFVFLDLNVLINHTLRQPKQORNAEV-RRALMWVCTVLAVFV 242
QY 247 ICFVFFHFARPYTLQSDRDVDTAENTLFYVKESTIMLTSLNACLDPFIYFPLCKSFR 306
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D1CFVPHMVQLPWTLAEL-GWPPSSNHQAINDAHQVTLCLLSTNCVLDPVLYCFLTKKFR 301
QY 307 NSLISMLKCPNSATSLSDNRKKQDGDPEETPM 342
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D302 KHLSEKLIMRSSQKCSRVTDTGTGEMAIPINHTEPV 337
```

```
RESULT 13
EBI2 HUMAN
ID EBI2 HUMAN STANDARD; PRT; 361 AA.
AC P32249;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE EBV-induced G protein-coupled receptor 2 (EBI2).
GN EBI2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yamamanchili R.R., Lenoir G.M.,
RA Kieff E.;
RA "Epstein-Barr virus-induced genes: first lymphocyte-specific G
```

```
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
CC -!- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
CC LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
CC -!- TISSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
CC -!- INDUCTION: BY EBV.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
CC -----
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CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L08177; AAA35924.1; .
DR PIR; B45680; B45680.
DR Genew; HGNC:3128; EBI2.
DR MIM; 605741; .
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; TAS.
DR GO; GO:0006955; P:immune response; TAS.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00237; GPCRHOOPS.
DR PROSITE; PS00237; G-PROTEIN RECF_F1_1; 1.
DR PROSITE; PS0262; G-PROTEIN RECF_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 32 57 1 (POTENTIAL).
FT DOMAIN 58 77 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 78 95 2 (POTENTIAL).
FT DOMAIN 96 105 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 106 127 3 (POTENTIAL).
FT DOMAIN 128 149 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 150 168 4 (POTENTIAL).
FT DOMAIN 169 192 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 193 215 5 (POTENTIAL).
FT DOMAIN 216 241 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 242 265 6 (POTENTIAL).
FT DOMAIN 266 287 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 288 312 7 (POTENTIAL).
FT DOMAIN 313 361 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 126 134 INTERACTION WITH G PROTEINS.
FT DISULFID 104 181 BY SIMILARITY.
SQ SEQUENCE 361 AA; 41224 MW; B5A2171F34C9C67B CRC64;

Query Match 21.3%; Score 379.5; DB 1; Length 361;
Best Local Similarity 26.0%; Pred. No. 8.6e-20;
Matches 94; Conservative 84; Mismatches 152; Indels 31; Gaps 11;

QY 1 MQAVDNLT----SAPGNTSLCTRDYKITQVLFPFLYTVLVFVGLITGLAMRIFFQIRSK 56
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D3 IQMANNFTPPSATPQGNDCDLVAHHSSTARIVWPLHYSLVFIIGLVNLLALVIVQNRKK 62
QY 57 SN-FIIFLKNVVISDLLMILTFPPKIL-----SDAKLGTGLRFLVFCQVTSVIFYFTMYI 110
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D63 INSTLYTNLVISDLITFTLPTLPTIAYYAMGFWRIGDA-----LCRITALVFYINTYA 117
QY 111 SISFLGLITIDRYOKTRPEKTSNPKNLGAKILSVVIAFWFLSLPNI--LTNRQPR 168
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D118 GYNFTCLSIDRFIAVHPLRVNKKRIEHAQGVCFVAILVFAQTLELLINPMKQBAE 177
QY 169 DKNVKKCSFLKSEFGLVWHEIYVNIQVIFNFIIVICVTLITKELYRS-----YVRT 223
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D178 RITCMYEYFNFEETKSLPW--ILLGACFIYGVLPILILICYSQICKLFRKAKNPLTEK 235
QY 224 RGVGKVPKKNVKNVFIILIAVFFICFVPHFARIPYTLISQTR--DVFDCTAENTLIFYVKE 281
D : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
D236 SGVYK---KALNT-IILIVVFLCTFYHVAIQHMIKKLRFNSFLECSQRHSFQISLH 291
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QY 282 STLWLTSLNACLDPTLYFFLCKSPNSLISMLKCPNSATISLQDNRRKKEQDGGDPNETP 341
Db 292 FTVCLMNFNCCDDPTLYFFACKYRKKVRMLK-RQVSVSISAVKSPNSREMTETQ 350
QY 342 M 342
Db 351 M 351

RESULT 14
ID CLT2_PIG STANDARD; PRT; 345 AA.
AC Q95N03;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cysteinyln leukotriene receptor 2 (CysLTR2).
GN CysLTR2 OR CysLTR2.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Kamohara M., Takasaki J., Matsumoto M., Matsumoto S., Saito T.,
RA Chishi T., Soga T., Matsushime H., Furuichi K.;
RT "Characterization of the cloned rat and porcine cysteinyl leukotriene
RT receptors."
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC mediating via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (by similarity).
CC -!- FUNCTION: Receptor for cysteinyl leukotrienes. The response is
CC mediated via a G-protein that activates a phosphatidylinositol-
CC calcium second messenger system (by similarity).
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; AB052662; BAB60817.1;
CC InterPro; IPR004071; GysLeuk_receptor.
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PRO1533; CysLTR2RCPT.
CC PRINTS; PRO0237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN RECEPTOR F1.1; FALSE_NEG.
CC PROSITE; PS00262; G-PROTEIN RECEPTOR F1.2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 43 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 44 64 1 (POTENTIAL).
FT DOMAIN 65 73 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 74 94 2 (POTENTIAL).
FT DOMAIN 95 124 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 125 145 3 (POTENTIAL).
FT DOMAIN 146 154 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 155 175 4 (POTENTIAL).
FT DOMAIN 176 205 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 206 226 5 (POTENTIAL).
FT DOMAIN 227 246 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 247 267 6 (POTENTIAL).
FT DOMAIN 268 297 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 298 308 7 (POTENTIAL).
FT DOMAIN 309 345 CYTOPLASMIC (POTENTIAL).
FT DISULFID 112 188 BY SIMILARITY.
FT CARBOHYD 20 20 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 184 184 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 345 AA; 39410 MW; 5D1B1FB98BB95905 CRC64;

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Query Match 20.6%; Score 367; DB 1; Length 345;
Best Local Similarity 29.0%; Pred. No. 6.le-19;
Matches 93; Conservative 72; Mismatches 134; Indels 22; Gaps 9;

QY 1 MQAVDNLTGAPGNTSLCTRDYKITQVFLPFLLYTLVFFVGLITNGLAMRIFFOIRSKSNFI 60
Db 17 MEENSTLGHNSNRSCCTTENPK--REFYIVLVIFINGALNGFSGIYVFLPKPKSTSV 74

QY 61 -FLKNTVISDLMLITLTPPKI-----LSDAKLGTGRLPTFVCQVTSVIFVTMTISISF 114
Db 75 NVFEMNLAIISDLITLFTTLEFRVYVYLRGNSXIFGDT-----CRMSYSMYNMYSSYF 129

QY 115 LGLITIDRYQKTRPPKTSNPKNLLGAKILSVVIAFWAFMLLSPNNILTNPRQDKNVKK 174
Db 130 LTVLVVVRFLATVHPRLHTTSIKNANLLCGVW--IFIMASSTVLLKNGSEQKDNVTL 187

QY 175 CSFLKSEFGLVWHEIVNYICQVI-FWINEFLIVIVCYTLTKELYRSYVTRGVGKVPKPK 233
Db 188 CLELNSN-KVTKLTNNYVALVGVFLPFGTSLICYLLIIRALLKVEVPESGL-RLSHRK 245

QY 234 VNVKVFIIIAVFICFVPFHARIPVYLSQTRDVFDCDAENTLFVVKESTLMTLSINACL 293
Db 246 ALITVIALIIILCLPLPYHVTHTLLEWKAD----KCKORLHKAVAVTLALAAANSFC 301

QY 294 DPFYFFLCKSPNSLISMLK 314
Db 302 NPFLYFAGENFKDLKSLAR 322

RESULT 15
ID PAFR_MOUSE STANDARD; PRT; 341 AA.
AC Q62035;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129/Sv;
RX MEDLINE=96239129; PubMed=8670084;
RA Ishii S., Matsuda Y., Nakamura M., Waga I., Kume K., Izumi T.,
RA Noma M., Shimizu T.;
RT "A murine platelet-activating factor receptor gene: cloning,
RT chromosomal localization and up-regulation of expression by
RT lipopolysaccharide in peritoneal resident macrophages.";
RL Biochem J 314:671-678(1996)
CC -!- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
CC MUSCLE CONTRACTIONS AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
CC ACTION VIA A G PROTEIN THAT ACTIVATES A PHOSPHATIDYLINOSITOL-
CC CALCIUM SECOND MESSENGER SYSTEM.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC
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CC
CC EMBL; D50872; BAA09468.1;
CC PIR; S63666; S63666.
CC MGD; MGI:106066; Ptafr.
CC InterPro; IPR000276; GPCR_Rhodpsn.

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Search completed: February 4, 2004, 14:29:33  
Job time : 19 secs